

GenCore version 5.1.4 p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:46:26 ; Search time 278.727 Seconds
(without alignments)
2192.677 Million cell updates/sec

Title: US-09-270-437D-9
Perfect score: 21
Sequence: 1 gaagatctcttaaggacgcc 21
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

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9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

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18: em.in.*

19: em.mu.*

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21: em.or.*

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37: em.htg.vrt.*

38: em.sv.*

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40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	21	100.0	1740	6	AX365954	AX365954 Sequence
2	21	100.0	1743	6	AX366054	AX366054 Sequence
3	21	100.0	1743	6	AX366057	AX366057 Sequence
4	21	100.0	1764	6	AX366035	AX366035 Sequence
5	21	100.0	4155	9	HSU76705	U76705 Human putat
6	21	100.0	4159	6	ARI71863	ARI71863 Sequence
7	21	100.0	4171	9	AF117108	AF117108 Homo sapi
8	21	100.0	4181	6	AX333233	AX333233 Sequence
9	21	100.0	4181	6	AX365782	AX365782 Sequence
10	21	100.0	4181	6	HSU97188	U97188 Homo sapien
11	21	100.0	4602	6	AX397963	AX397963 Sequence
12	21	100.0	51119	2	AC090865	AC090865 Homo sapi
13	21	100.0	54379	9	AC079780	AC079780 Homo sapi
14	21	100.0	57261	2	AC090245	AC090245 Homo sapi
15	21	100.0	176547	9	AC092447	AC092447 Homo sapi
16	21	100.0	182312	2	AC087709	AC087709 Homo sapi
17	21	100.0	188389	2	AC024199	AC024199 Homo sapi
18	18.4	87.6	1740	10	AB046173	AB046173 Mus muscu
19	18.4	87.6	192406	2	AC115321	AC115321 Rattus no
20	17.8	84.8	60096	2	AC114540	AC114540 Mus muscu
21	17.8	84.8	109198	8	AC078891	AC078891 Oryza sat
22	17.8	84.8	129432	9	HS497321	AL023775 Human DNA
23	17.4	82.9	104983	2	AC119590	AC119590 Rattus no
24	17.4	82.9	167274	2	AC112310	AC112310 Rattus no
25	17.4	82.9	260605	2	AC099211	AC099211 Rattus no
26	17	81.0	143498	9	AC105391	AC105391 Homo sapi
27	17	81.0	159768	2	AC118170	AC118170 Rattus no
28	17	81.0	176348	2	AC102550	AC102550 Mus muscu
29	17	81.0	177435	2	AC128321	AC128321 Rattus no
30	17	81.0	194235	2	AC102586	AC102586 Mus muscu
31	17	81.0	201474	2	AC127286	AC127286 Mus muscu
32	16.8	80.0	2759	8	TGSUCSYN1	X96938 T.gesnerian
33	16.8	80.0	7661	10	AF012923	AF012923 Mus muscu
34	16.8	80.0	31170	3	CEF35E12	Z81527 Caenorhabdi
35	16.8	80.0	35016	9	AL603838	AL603838 Human DNA
36	16.8	80.0	81954	2	AC015133	AC015133 Drosophil
37	16.8	80.0	102477	2	AC110687	AC110687 Rattus no
38	16.8	80.0	114382	2	AC103498	AC103498 Rattus no
39	16.8	80.0	128750	2	AC007307	AC007307 Mus muscu
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41	16.8	80.0	132171	3	AC008370	AC008370 Drosophil
42	16.8	80.0	133273	2	AC068586	AC068586 Homo sapi
43	16.8	80.0	133273	2	AC068586	AC068586 Homo sapi
44	16.8	80.0	140186	2	AC055808	AC055808 Homo sapi
45	16.8	80.0	157559	2	AC020344	AC020344 Drosophil

ALIGNMENTS

RESULT 1
AX365954
LOCUS
DEFINITION
Sequence 347 from Patent WO0200174.
ACCESSION
AX365954
VERSION
AX365954.1 GI:18697455
KEYWORDS
human.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Wang T., Wang A., Skeiky Y.A., Li S.X., Kalos M.D., Henderson R.A.,
McNeill P.D., Fanger N., Retter M.W., Marnerakis M., Fanger G.R.,
Vedvick T.S., Carter D., Watanabe Y. and Peckham D.W.

TITLE Compositions and methods for the therapy and diagnosis of lung

JOURNAL cancer
Patent: WO 0200174-A 347 03-JAN-2002;
CORIXA CORPORATION (US)

FEATURES Location/Qualifiers
source 1..1740

BASE COUNT 526 a 406 c 417 g 391 t
ORIGIN /db_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 3.3; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21

Db 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 2
AX366054 1743 bp DNA linear PAT 15-FEB-2002

LOCUS AX366054 Sequence 447 from Patent WO0200174.

DEFINITION AX366054

ACCESSION AX366054.1 GI:18697498

VERSION

KEYWORDS human.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT 527 a 406 c 418 g 392 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 3

AX366057 1743 bp DNA linear PAT 15-FEB-2002

LOCUS AX366057 Sequence 450 from Patent WO0200174.

DEFINITION AX366057

ACCESSION AX366057.1 GI:18697500

VERSION

KEYWORDS human.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT 526 a 406 c 417 g 391 t

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RESULT 4

AX366035 1764 bp DNA linear PAT 15-FEB-2002

LOCUS AX366035 Sequence 428 from Patent WO0200174.

DEFINITION AX366035

ACCESSION AX366035.1 GI:18697484

VERSION

KEYWORDS human.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT 527 a 406 c 418 g 392 t

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Query Match 100.0%; Score 21; DB 6; Length 1764;

Best Local Similarity 100.0%; Pred. No. 3.3;

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RESULT 5

HSU76705 4155 bp mRNA linear PRI 26-JAN-1999

LOCUS HSU76705 Human putative RNA binding protein Koc1 mRNA, complete cds.

DEFINITION U76705

ACCESSION U76705.1 GI:4098296

VERSION

KEYWORDS Homo sapiens.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT 534 a 417 c 419 g 394 t

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 1764;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21

Db 76 GAAAGTATCTTCAAGGACGCC 96

RESULT 5

HSU76705 4155 bp mRNA linear PRI 26-JAN-1999

LOCUS HSU76705 Human putative RNA binding protein Koc1 mRNA, complete cds.

DEFINITION U76705

ACCESSION U76705.1 GI:4098296

VERSION

KEYWORDS Homo sapiens.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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BASE COUNT 534 a 417 c 419 g 394 t

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ACCESSION U76705.1 GI:4098296

VERSION

KEYWORDS Homo sapiens.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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Db 76 GAAAGTATCTTCAAGGACGCC 96

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HSU76705 4155 bp mRNA linear PRI 26-JAN-1999

LOCUS HSU76705 Human putative RNA binding protein Koc1 mRNA, complete cds.

DEFINITION U76705

ACCESSION U76705.1 GI:4098296

VERSION

KEYWORDS Homo sapiens.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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BASE COUNT 534 a 417 c 419 g 394 t

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Db 76 GAAAGTATCTTCAAGGACGCC 96

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HSU76705 4155 bp mRNA linear PRI 26-JAN-1999

LOCUS HSU76705 Human putative RNA binding protein Koc1 mRNA, complete cds.

DEFINITION U76705

ACCESSION U76705.1 GI:4098296

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REFERENCE

AUTHORS

TITLE

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BASE COUNT 534 a 417 c 419 g 394 t

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HSU76705 4155 bp mRNA linear PRI 26-JAN-1999

LOCUS HSU76705 Human putative RNA binding protein Koc1 mRNA, complete cds.

DEFINITION U76705

ACCESSION U76705.1 GI:4098296

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KEYWORDS Homo sapiens.

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ORGANISM

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AUTHORS

TITLE

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BASE COUNT 534 a 417 c 419 g 394 t

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LOCUS HSU76705 Human putative RNA binding protein Koc1 mRNA, complete cds.

DEFINITION U76705

ACCESSION U76705.1 GI:4098296

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HSU76705 4155 bp mRNA linear PRI 26-JAN-1999

LOCUS HSU76705 Human putative RNA binding protein Koc1 mRNA, complete cds.

DEFINITION U76705

ACCESSION U76705.1 GI:4098296

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KEYWORDS Homo sapiens.

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGTATCTTCAAGGACGCC 21
Db 305 GAAAGTATCTTCAAGGACGCC 325
RESULT 6
LOCUS AR171863 4159 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 4 from patent US 6297364.
ACCESSION AR171863
VERSION AR171863.1 GI:17910813
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4159)
AUTHORS Chen,Y.-T., Gure,A., Tsang,S., Stockert,E., Jager,E., Alexander,K.
and Old,L.J.
TITLE Isolated nucleic acid molecule encoding cancer associated antigen,
the antigen itself, and uses thereof
JOURNAL Patent: US 6297364-A 4 02-OCT-2001;
FEATURES
Location/Qualifiers
source 1..4159
/organism="unknown"
BASE COUNT 1281 a 830 c 851 g 1181 t 16 others
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Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGTATCTTCAAGGACGCC 21
Db 305 GAAAGTATCTTCAAGGACGCC 325
RESULT 7
LOCUS AF117108 4171 bp mRNA linear PRI 26-JAN-1999
DEFINITION Homo sapiens IGF-II mRNA-binding protein 3 (IMP-3) mRNA, complete
cds.
ACCESSION AF117108
VERSION AF117108.1 GI:4191611
KEYWORDS
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4171)
AUTHORS Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H.,
Wewer,U.M. and Nielsen,F.C.
TITLE A family of insulin-like growth factor II mRNA-binding proteins
represses translation in late development
JOURNAL Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
MEDLINE 99108099
PUBMED 9891060
REFERENCE 2 (bases 1 to 4171)
AUTHORS Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H.,
Wewer,U.M. and Nielsen,F.C.
Direct Submission
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
FEATURES
Location/Qualifiers
source 1..4171
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/db_xref="taxon:9606"
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267..2006
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cancer (koc)"
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Best Local Similarity 100.0%; Pred. No. 3.3;
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QY 1 GAAAGTATCTTCAAGGACGCC 21
Db 321 GAAAGTATCTTCAAGGACGCC 341
RESULT 8
LOCUS AX333233 4181 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 3742 from Patent WO0194629.
ACCESSION AX333233
VERSION AX333233.1 GI:18123867
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horzigan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3742 13-DEC-2001;
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FEATURES             Avalon Pharmaceuticals (US)
source               Location/Qualifiers
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGAGGCC 21
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Db 305 GAAAGTATCTTCAAGGAGGCC 325

RESULT 9
AX365782             4181 bp DNA linear PAT 15-FEB-2002
DEFINITION           Sequence 175 from Patent WO0200174.
ACCESSION             AX365782
VERSION               AX365782.1 GI:18697320
KEYWORDS              human.
SOURCE                Homo sapiens
ORGANISM              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS              Wang, T., Wang, A., Skeiky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A.,
                      McNeill, P.D., Fanger, N., Retter, M.W., Marnerakis, M., Fanger, G.R.,
                      Vedvick, T.S., Carter, D., Watanabe, Y. and Pecham, D.W.
TITLE                Compositions and methods for the therapy and diagnosis of lung
                      cancer
JOURNAL              Patent: WO 0200174-A 175 03-JAN-2002;
                      CORIXA CORPORATION (US)
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 305 GAAAGTATCTTCAAGGAGGCC 325

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HSU97188             4181 bp mRNA linear PRI 11-SEP-1998
LOCUS                HSD97188
DEFINITION           Homo sapiens putative RNA binding protein KOC (koc) mRNA, complete
                      cds.
ACCESSION             U97188
VERSION               U97188.1 GI:2105468
KEYWORDS              Homo sapiens.
SOURCE                Homo sapiens
ORGANISM              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS              Mueller-Pillasch, F., Lacher, U., Wallrapp, C., Micha, A.,
                      Zimmerhackl, F., Hameister, H., Varga, G., Friess, H., Buchler, M.,
                      Beger, H.G., Vila, M.R., Adler, G. and Gress, T.M.
TITLE                Cloning of a gene highly overexpressed in cancer coding for a novel
                      KH-domain containing protein
JOURNAL              Oncogene 14 (22), 2729-2733 (1997)
MEDLINE              97322117
PUBMED              9178771

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REFERENCE            2 (bases 1 to 4181)
AUTHORS              Mueller-Pillasch, F., Lacher, U., Wallrapp, C., Micha, A.,
                      Zimmerhackl, F., Hameister, H., Varga, G., Friess, H., Buchler, M.,
                      Beger, H.G., Vila, M.R., Adler, G. and Gress, T.M.
TITLE                Direct Submission
JOURNAL              Submitted (11-APR-1997) Medizinische Klinik, Internal Medicine I,
                      Robert-Koch-Str. 8, Ulm 89081, Germany
FEATURES             Location/Qualifiers
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                     /protein_id="AAC35208.1"
                     /db_xref="GI:2105469"
                     /translation="MNKLYIGNLSNAAAPSDLESIFDKAKIPVSGPFLVTKGYAFVDC
                      PDESWALKAIRALSGKIELHGKPIEVHSVPKQRIKQIRNIPPHLQWEVLDSLLV
                      QGVVSECEQVNTDSETAVNVYSSKQARQALDKLNGFLENFTLVAVIYIPDMAA
                      QCNPLQQRGRGLGQRRSGSGSKQPCDPLRLIAPVTOFVGAIIGKAGATI
                      RNITKQTKIDVHKNAGAEKSTITLSTPEGSAAKSLILEMHKEAQDIKTEE
                      IPLKILAHNFVRLIGKEGRNLKKIEQDTDTKITISPLQELTLNPTITVKNVE
                      TCABEESIMKKIRSEYENDIASMNLQAHILPGLNIALGLFPPTSGMPPPTSGPPSA
                      MTPPYQEQSETETVHOFIPALSVGAIIGKQGHIKOLSRFAGASIKIAPAEAPDAK
                      VRMLITGPPEAKQACQRIYGIKEENFVSPKEVLEAHIRVFSFAAGRVIGKGGK
                      TVNELQSSAEVVPVPTQTPDNDQVVVKITGHFYACQVAKQKIEILTVQKQHQQ
                      KALQSGPPQSRKK"
BASE COUNT          1303 a 830 c 851 g 1181 t 16 others
ORIGIN
Query Match          100.0%; Score 21; DB 9; Length 4181;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGAGGCC 21
|||||
Db 305 GAAAGTATCTTCAAGGAGGCC 325

RESULT 11
AX397963             4602 bp DNA linear PAT 27-MAY-2002
LOCUS                AX397963
DEFINITION           Sequence 1 from Patent WO0220036.
ACCESSION             AX397963
VERSION               AX397963.1 GI:21260818
KEYWORDS              human.
SOURCE                Homo sapiens
ORGANISM              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS              Mueller, F., Gress, T. and Adler, G.
TITLE                Medicament comprising a dna sequence, which codes for the
                      rna-binding koc protein, and comprising a koc protein or a dna
                      sequence of the koc promoter
JOURNAL              Patent: WO 0220036-A 1 14-MAR-2002;
                      Mueller, Friederike (DE)
FEATURES             Location/Qualifiers
source               1..4602
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     672..2411
                     /note="unnamed protein product"

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Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project information
Center project name: L13138
Center clone name: 494_F_2

* NOTE: This record contains 61 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

769	868:	gap of	100	bp
869	1537:	contig of	729	bp in length
1598	1697:	gap of	100	bp
1698	2452:	contig of	755	bp in length
2453	2552:	gap of	100	bp
2553	3234:	contig of	742	bp in length
3295	3394:	gap of	100	bp
3395	4151:	contig of	757	bp in length
4152	4251:	gap of	100	bp
4252	4995:	contig of	744	bp in length
4996	5095:	gap of	100	bp
5096	5948:	contig of	753	bp in length
5949	5948:	gap of	100	bp
5949	6689:	contig of	741	bp in length
6690	6789:	gap of	100	bp
6790	7531:	contig of	742	bp in length
7532	7631:	gap of	100	bp
7632	8361:	contig of	730	bp in length
8362	8461:	gap of	100	bp
8462	9202:	contig of	741	bp in length
9203	9302:	gap of	100	bp
9303	10050:	contig of	748	bp in length
10051	10150:	gap of	100	bp
10151	10868:	contig of	718	bp in length
10869	10968:	gap of	100	bp
10969	11718:	contig of	750	bp in length
11719	11818:	gap of	100	bp
11819	12541:	contig of	723	bp in length
12542	12641:	gap of	100	bp
12642	13349:	contig of	708	bp in length
13350	13449:	gap of	100	bp
13450	14174:	contig of	725	bp in length
14175	14274:	gap of	100	bp
14275	14996:	contig of	722	bp in length
14997	15096:	gap of	100	bp
15097	15827:	contig of	731	bp in length
15828	15927:	gap of	100	bp
15928	16677:	contig of	750	bp in length
16678	16777:	gap of	100	bp
16778	17496:	contig of	719	bp in length
17497	17596:	gap of	100	bp
17597	18342:	contig of	746	bp in length
18343	18442:	gap of	100	bp
18443	19193:	contig of	751	bp in length
19194	19293:	gap of	100	bp
19294	20044:	contig of	751	bp in length
20045	20144:	gap of	100	bp
20145	20872:	contig of	728	bp in length
20873	20972:	gap of	100	bp
20973	21715:	contig of	743	bp in length
21716	21815:	gap of	100	bp
21816	22554:	contig of	732	bp in length
22548	22647:	gap of	100	bp
22648	23401:	contig of	754	bp in length

RESULT 12	AC090865	5119 bp	DNA	linear	HTG 13-APR-2001
LOCUS	AC090865				
DEFINITION	Homo sapiens chromosome 15 clone RP11-494F2.map 15, LOW-PASS SEQUENCE SAMPLING.				
ACCESSION	AC090865				
VERSION	AC090865.2	GI:13621281			
KEYWORDS	HTG; HTGS PHASE0.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 5119)				
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.				
TITLE	Homo sapiens chromosome 15, clone RP11-494F2				

Unpublished
2 (bases 1 to 5119)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barna, N., Batiien, V., Boguelavkiy, L., Boukgalcer, B., Brown, A.,
Camata, J., Campopiano, A., Choepei, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Fato, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,
Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T.,
Lehoczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P.,
Marquies, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,
McPheters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, I., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schubback, R., Seaman, S., Severy, P.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Triglio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

TITLE
 Direct Submission
JOURNAL
 Submitted (11-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT
 On April 13, 2001 this sequence version replaced gi:13273446.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>.
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research

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* 23402 23501: gap of 100 bp
* 23502 24255: contig of 754 bp in length
* 24256 24355: gap of 100 bp
* 24356 25124: contig of 769 bp in length
* 25125 25224: gap of 100 bp
* 25225 25962: contig of 738 bp in length
* 25963 26062: gap of 100 bp
* 26063 26786: contig of 724 bp in length
* 26787 26886: gap of 100 bp
* 26887 27593: contig of 707 bp in length
* 27594 27693: gap of 100 bp
* 27694 28439: contig of 746 bp in length
* 28440 28539: gap of 100 bp
* 28540 29277: contig of 738 bp in length
* 29278 29377: gap of 100 bp
* 29378 30137: contig of 760 bp in length
* 30138 30237: gap of 100 bp
* 30238 30968: contig of 731 bp in length
* 30969 31068: gap of 100 bp
* 31069 31795: contig of 727 bp in length
* 31796 31895: gap of 100 bp
* 31896 32638: contig of 743 bp in length
* 32639 32738: gap of 100 bp
* 32739 33497: contig of 759 bp in length
* 33498 33597: gap of 100 bp
* 33598 34339: contig of 742 bp in length
* 34340 34439: gap of 100 bp
* 34440 35167: contig of 728 bp in length
* 35168 35267: gap of 100 bp
* 35268 36015: contig of 748 bp in length
* 36016 36115: gap of 100 bp
* 36116 36878: contig of 763 bp in length
* 36879 36978: gap of 100 bp
* 36979 37744: contig of 766 bp in length
* 37745 37844: gap of 100 bp
* 37845 38596: contig of 752 bp in length
* 38597 38696: gap of 100 bp
* 38697 39433: contig of 737 bp in length
* 39434 39533: gap of 100 bp
* 39534 40286: contig of 753 bp in length
* 40287 40386: gap of 100 bp
* 40387 41064: contig of 678 bp in length
* 41065 41164: gap of 100 bp
* 41165 41895: contig of 731 bp in length
* 41896 41995: gap of 100 bp
* 41996 42740: contig of 745 bp in length
* 42741 42840: gap of 100 bp
* 42841 43593: contig of 753 bp in length
* 43594 43693: gap of 100 bp
* 43694 44422: contig of 729 bp in length
* 44423 44522: gap of 100 bp
* 44523 45270: contig of 748 bp in length
* 45271 45370: gap of 100 bp
* 45371 46108: contig of 738 bp in length
* 46109 46208: gap of 100 bp
* 46209 46923: contig of 715 bp in length
* 46924 47023: gap of 100 bp
* 47024 47753: contig of 730 bp in length
* 47754 47853: gap of 100 bp
* 47854 48595: contig of 742 bp in length
* 48596 48695: gap of 100 bp
* 48696 49432: contig of 737 bp in length
* 49433 49532: gap of 100 bp
* 49533 50267: contig of 735 bp in length
* 50268 50367: gap of 100 bp
* 50368 51119: contig of 752 bp in length.

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FEATURES
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   /db_xref="taxon:9606"
   /chromosome="15"
   /map="15"
   /clone="RP11-494F2"

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BASE COUNT 12444 a 10521 c 9576 g 11843 t 6735 others
ORIGIN

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Query Match 100.0%; Score 21; DB 2; Length 51119;
Best Local Similarity 100.0%; Pred. No. 3.5; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

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Qy 1 GAAAGTATCTTCAAGGACGCC 21
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Db 28678 GAAAGTATCTTCAAGGACGCC 28698
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RESULT 13
AC079780/c

```

LOCUS AC079780 54379 bp DNA linear PRI 21-FEB-2002
DEFINITION Homo sapiens BAC clone RP11-379L16 from 7, complete sequence.
ACCESSION AC079780
VERSION AC079780.6 GI:18072220
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE 1 (bases 1 to 54379)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074

```

```

REFERENCE 2 (bases 1 to 54379)
AUTHORS Swearingen,S., Meyer,R. and Cotton,M.
TITLE The sequence of Homo sapiens BAC clone RP11-379L16
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 54379)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

```

```

REFERENCE 4 (bases 1 to 54379)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

```

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REFERENCE 5 (bases 1 to 54379)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

```

```

COMMENT On Jan 6, 2002 this sequence version replaced gi:17298647.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu
----- Summary Statistics
-----
Center project name: H_NH0379L16

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frangen, E., Tateno, M., Catanese, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is GSI-117B4, 2000 bp overlap; the clone sequenced to the right is GSI-13M19, 2000 bp overlap. Actual start of this clone is at base position 25835 of GSI-117B4; actual end is at base position 49313 of GSI-13M19.

Polymorphisms have been identified between AC023105 and AC079780.

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7"

/clone="RP11-379L16"
/clone_lib="RPCI-11"

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1. .70

repeat_region

72..370

repeat_region

382..809

misc_feature

795..1200

/notes="match to EST BG003407 (NID:gl2443713)"

repeat_region

1150..1454

repeat_region

1516..1628

repeat_region

1802..1840

repeat_region

/rpt_family="L1"

repeat_region

2087..2289

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repeat_region

2447..2725

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repeat_region

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repeat_region

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repeat_region

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7782..8020
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10461..10592
/rpt_family="L1"
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/rpt_family="Alu"
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11238..11512
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repeat_region
12292..12312
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12932..12965
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12938..13246
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13247..13341
/rpt_family="Alu"
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/notes="match to EST AA301911 (NID:gl954244)"
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13552..13836
/rpt_family="Alu"
repeat_region
13849..13892
/rpt_family="(T)n"

Query Match

100.0%; Score 21; DB 9; Length 54379;
Best Local Similarity -100.0%; Pred.No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon Apr 21 10:30:47 2003

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QY      1  GAAAGTATCTTCAAGACGCC 21
      |||||
Db 34372 GAAAGTATCTTCAAGACGCC 34352

RESULT 14
AC090245/c
LOCUS   Homo sapiens chromosome 18 clone RP11-888I12 map 18, LOW-PASS
DEFINITION
SEQUENCE SAMPLING.
ACCESSION AC090245
VERSION   2
KEYWORDS HTG; HTGS_PHASE0.
SOURCE   Homo sapiens.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 57261)
  Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
  Barna, N., Bastien, V., Boguslavskiy, L., Bouckgalter, B., Brown, A.,
  Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,
  Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
  Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,
  Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
  Hages, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
  Jones, C., Karatas, A., Latorque, K., Lamazares, R., Landers, T.,
  Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,
  Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,
  McPheters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
  Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
  O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
  Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
  Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
  Roy, A., Santos, R., Schauer, S., Schuppback, R., Seaman, S., Severy, P.,
  Sounez, C., Spencer, B., Stange-Thumann, N., Stojanovic, N.,
  Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
  Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
  Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
  Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 17, 2001 this sequence version replaced gi:12957879.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12326
Center clone name: 888_I_12
-----
* NOTE: This record contains 71 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1
* 717: contig of 717 bp in length
* 718 817: gap of 100 bp

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```

* 30633 30732: gap of 100 bp
* 30733 31440: contig of 708 bp in length
* 31441 31540: gap of 100 bp
* 31541 32256: contig of 716 bp in length
* 32257 32356: gap of 100 bp
* 32357 33051: contig of 695 bp in length
* 33052 33151: gap of 100 bp
* 33152 33864: contig of 713 bp in length
* 33865 33964: gap of 100 bp
* 33965 34677: contig of 713 bp in length
* 34678 34777: gap of 100 bp
* 34778 35494: contig of 717 bp in length
* 35495 35594: gap of 100 bp
* 35595 36312: contig of 718 bp in length
* 36313 36412: gap of 100 bp
* 36413 37086: contig of 674 bp in length
* 37087 37186: gap of 100 bp
* 37187 37877: contig of 691 bp in length
* 37878 37977: gap of 100 bp
* 37978 38681: contig of 704 bp in length
* 38682 38781: gap of 100 bp
* 38782 39450: contig of 669 bp in length
* 39451 39550: gap of 100 bp
* 39551 40238: contig of 688 bp in length
* 40239 40338: gap of 100 bp
* 40339 41055: contig of 717 bp in length
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* 41974 42694: contig of 721 bp in length
* 42695 42794: gap of 100 bp
* 42795 43495: contig of 701 bp in length
* 43496 43595: gap of 100 bp
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* 44321 44420: gap of 100 bp
* 44421 45137: contig of 707 bp in length
* 45128 45227: gap of 100 bp
* 45228 45922: contig of 705 bp in length
* 45933 46032: gap of 100 bp
* 46033 46734: contig of 702 bp in length
* 46735 46834: gap of 100 bp
* 46835 47535: contig of 701 bp in length
* 47536 47635: gap of 100 bp
* 47636 48346: contig of 711 bp in length
* 48347 48446: gap of 100 bp
* 48447 49130: contig of 684 bp in length
* 49131 49230: gap of 100 bp
* 49231 49954: contig of 724 bp in length
* 49955 50054: gap of 100 bp
* 50055 50770: contig of 716 bp in length
* 50771 50870: gap of 100 bp
* 50871 51594: contig of 724 bp in length
* 51595 51694: gap of 100 bp
* 51695 52402: contig of 708 bp in length
* 52403 52502: gap of 100 bp
* 52503 53213: contig of 711 bp in length
* 53214 53313: gap of 100 bp
* 53314 54026: contig of 713 bp in length
* 54027 54126: gap of 100 bp
* 54127 54831: contig of 705 bp in length
* 54832 54931: gap of 100 bp
* 54932 55624: contig of 693 bp in length

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Query Match      100.0%; Score 21; DB 2; Length 57261;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAAAGTATCTTCAAGGACGCC 21
DB 28686 GAAAGTATCTTCAAGGACGCC 28666

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RESULT 15

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AC092447
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

```

```

AC092447
Homo sapiens BAC clone RP11-760D2 from 7, complete sequence.
AC092447
AC092447.5 GI:18873962
HTG
Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176547)
Sulston, J.B. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
9847074
2 (bases 1 to 176547)
Armstrong, J. and Cotton, M.
The sequence of Homo sapiens BAC clone RP11-760D2
Unpublished (2001)
3 (bases 1 to 176547)
Waterston, R.H.
Direct Submission
Submitted (04-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 176547)
Waterston, R.H.
Direct Submission
Submitted (23-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 176547)
Waterston, R.H.
Direct Submission
Submitted (27-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 23, 2002 this sequence version replaced gi:18259201.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0760D02
-----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>, send mailto:egreen@nhgri.nih.gov, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,

Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP13-492C18; the clone sequenced to the right is RP11-10F11. 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-760D2; actual end is at base position 17615 of RP11-10F11.

The region from 20341 to 20385 is covered only by a PCR product from clone DNA. An unresolved simple sequence repeats exists between 84203 and 84724. Polymorphisms exists between AC024199 and AC092447. Data from AC024199 and AC092423 was used to finish AC092447.

FEATURES
source
1. .176547
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7"
/clone="RP11-760D2"
/clone_lib="RPCI-11"
5. .1938
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2799..2962
/note="match to EST BF895059 (NID:G12286518)"
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3795..4263
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4259..4542
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4749..5046
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5047..5267
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5268..5560
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5561..6091
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6528..6825
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8380..8686
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8924..9225
/rpt_family="Alu"
9838..10125
/rpt_family="Alu"
10336..10600
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11975..12282
/rpt_family="Alu"
12457..12765
/rpt_family="Alu"
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/note="similar to Homo sapiens EST BF979990 (NID:G12347205)"

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/note="similar to Homo sapiens EST BE879245 (NID:G10328021)"
misc_feature
14412..14448
/note="similar to Homo sapiens EST AL520426 (NID:G12783919)"
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14530..14608
/rpt_family="L1"
repeat_region
14609..14910
/rpt_family="Alu"
repeat_region
14911..15079
/rpt_family="L1"
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15062..15811
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15812..16112
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16113..16529
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misc_feature
16530..16941
/note="similar to Homo sapiens EST AA446576 (NID:G2159241) zw84d02.81"
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16541..17068
/note="similar to Homo sapiens EST BE966979 (NID:G11772953)"
misc_feature
16586..17133
/note="similar to Homo sapiens EST BE622588 (NID:G9893515)"
misc_feature
16610..17149
/note="similar to Homo sapiens EST AI744560 (NID:G5112848) wg09g02.xl"
misc_feature
16743..17248
/note="similar to Homo sapiens EST N46675 (NID:G1187841) yy50c07.rl"
misc_feature
16912..17332
/note="similar to Homo sapiens EST AA446703 (NID:G2159368) zw84d02.rl"
misc_feature
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/note="match to EST BG479148 (NID:G13411427)"
misc_feature
17135..17383
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17144..17383
/note="similar to Homo sapiens EST BG480641 (NID:G13412920)"
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/rpt_family="L1"
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17826..18132
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17826..17839
/note="similar to Homo sapiens EST AA669082 (NID:G2630581) ab92h09.81"
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18142..18846
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misc_feature
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Query Match 100.0%; Score 21; DB 9; Length 176547;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
Db 167744 GAAAGTATCTTCAAGGACGCC 167764

Search completed: April 18, 2003, 06:15:49
Job time : 345.727 secs

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	21	100.0	21	21	AAZ36155	PCR primer	
2	21	100.0	1740	21	AAZ66035	Human lung	
3	21	100.0	1740	24	ABL49354	Human lung	
4	21	100.0	1743	24	ABL49357	Human lung	
5	21	100.0	1743	24	ABL49359	Human lung	
6	21	100.0	1764	24	ABL49283	Human lung	
7	21	100.0	4159	21	AAZ36150	DNA encoding	
8	21	100.0	4181	21	AAZ65900	Human lung	
9	21	100.0	4181	24	ABL65405	Lung cancer	

ALIGNMENTS

XX Nucleotides representing cancer-associated genes, used to develop
PT products for the diagnosis, monitoring and treatment of cancers
PT
yy

instant

CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 other;
SQ
Query Match 100.0%; Score 21; DB 21; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGTATCTTCAAGGAGGCC 21
DB 55 GAAAGTATCTTCAAGGAGGCC 75
RESULT 3
ABL49254
ID ABL49254 standard; cDNA; 1740 BP.
XX ABL49254;
AC ABL49254;
XX 01-MAY-2002 (first entry)
XX Human lung tumour L523S cDNA sequence SEQ ID NO:347.
XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
XX immune response; ss.
XX Homo sapiens.
XX WO200200174-A2.
XX 03-JAN-2002.
XX 28-JUN-2001; 2001WO-US21065.
XX 28-JUN-2000; 2000US-0606421.
XX 02-AUG-2000; 2000US-0630940.
XX 21-AUG-2000; 2000US-0643597.
XX 15-SEP-2000; 2000US-0662786.
XX 09-OCT-2000; 2000US-0685696.
XX 12-DEC-2000; 2000US-0735705.
XX 07-MAY-2001; 2001US-0850716.
XX (CORI-) CORIXA CORP.
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
XX McNeill PD, Fanger N, Retter MW, Warnerakis M, Fanger GR;
XX Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX WPI; 2002-090513/12.
XX P-PSDB; ABB74997.
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
XX lung cancer or stimulating an immune response -
XX Example 2; Page 330; 374pp; English.
XX The present invention describes human lung tumour proteins. Human lung
XX tumour proteins and polynucleotides have cytostatic and immunostimulant
XX activities, and can be used in vaccine production. Compositions
XX comprising the lung tumour proteins, polynucleotides, antibodies,
XX fusion proteins, T cell populations, or antigen presenting cells that
XX express the lung tumour proteins are useful for treating lung cancer or
XX stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
XX ABB75070 represent sequences used in the exemplification of the present
XX invention.
XX Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 other;
SQ

PS Claim 108; Page 13; 44pp; English.
XX PCR primers AA236155-56 were used to amplify a cancer associated antigen
CC gene designated KOC-1. The specification also describes a cancer
CC associated antigen designated CT7. The CT7 polynucleotide was isolated
CC from SK-MEL-37 melanoma cells. The polypeptide has some homology with
CC MAGE-10, limited to about 210 carboxy terminal amino acids. The amino
CC terminal of the protein has a repetitive pattern, with repeats rich in
CC serine, proline, glutamine and leucine, and an almost invariable core of
CC the peptide given in AYA43877. The CT7 polypeptide can be processed to
CC peptides which provoke lysis by cytolytic T cells. The polynucleotides
CC and polypeptides can be used for treating a cancerous condition and
CC screening for or diagnosing cancerous conditions. The cancer associated
CC antigens can be used as an immunogenic or vaccine composition with an
CC adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony
CC stimulating factor (GM-CSF).
XX Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGTATCTTCAAGGAGGCC 21
DB 1 GAAAGTATCTTCAAGGAGGCC 21
RESULT 2
AAC66035
ID AAC66035 standard; cDNA; 1740 BP.
XX AAC66035;
AC AAC66035;
XX 21-FEB-2001 (first entry)
XX Human lung cancer-associated cDNA antigen L523S.
XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX vaccine; detection; ss.
XX Homo sapiens.
XX WO2000061612-A2.
XX 19-OCT-2000.
XX 03-APR-2000; 2000WO-US08896.
XX 02-APR-1999; 99US-0285479.
XX 17-DEC-1999; 99US-0465396.
XX 30-DEC-1999; 99US-0476496.
XX 10-JAN-2000; 2000US-0480884.
XX 22-FEB-2000; 2000US-0510376.
XX (CORI-) CORIXA CORP.
XX Wang T, Fan L;
XX WPI; 2000-628399/60.
XX P-PSDB; AAB11365.
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
XX protein is used for detecting and monitoring progression of lung cancer
XX in a patient -
XX Claim 1a; Page 258-259; 261pp; English.
XX This invention describes a novel isolated polypeptide (I) which
XX comprising an immunogenic portion of a lung tumor protein or variant (P2)
XX which have cytostatic activity. The polypeptides and polynucleotides are
XX used in compositions and vaccines to inhibit the development of cancer,
XX especially lung cancer, in a patient. Methods described in the invention

Query Match 100.0%; Score 21; DB 24; Length 1740;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
 |||||
 DB 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 4
 ABL49297
 ID ABL49297 standard; cDNA; 1743 BP.
 XX
 AC ABL49297;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human lung tumour L523S recombinant polynucleotide SEQ ID NO:447.
 XX
 KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 KW immune response; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200174-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 28-JUN-2001; 2001WO-US21065.
 XX
 PR 28-JUN-2000; 2000US-0606421.
 PR 02-AUG-2000; 2000US-0630940.
 PR 21-AUG-2000; 2000US-0643597.
 PR 15-SEP-2000; 2000US-0662786.
 PR 09-OCT-2000; 2000US-0685696.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
 XX
 DR WPI; 2002-090513/12.
 DR P-PSDB; ABB75053.
 XX
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 XX
 PS Claim 1; Page 367; 374pp; English.
 XX
 CC The present invention describes human lung tumour proteins. Human lung
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 1743 BP; 527 A; 406 C; 418 G; 392 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 1743;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
 |||||
 DB 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 6
 ABL49283
 ID ABL49283 standard; cDNA; 1764 BP.
 XX
 AC ABL49283;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human lung tumour L523S recombinant polynucleotide SEQ ID NO:428.

RESULT 5
 ABL49299
 ID ABL49299 standard; cDNA; 1743 BP.
 XX
 AC ABL49299;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human lung tumour L523S recombinant polynucleotide SEQ ID NO:450.
 XX
 KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 KW immune response; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200174-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 28-JUN-2001; 2001WO-US21065.
 XX
 PR 28-JUN-2000; 2000US-0606421.
 PR 02-AUG-2000; 2000US-0630940.
 PR 21-AUG-2000; 2000US-0643597.
 PR 15-SEP-2000; 2000US-0662786.
 PR 09-OCT-2000; 2000US-0685696.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
 XX
 DR WPI; 2002-090513/12.
 DR P-PSDB; ABB75054.
 XX
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 XX
 PS Claim 1; Page 370; 374pp; English.
 XX
 CC The present invention describes human lung tumour proteins. Human lung
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 1743 BP; 527 A; 406 C; 418 G; 392 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 1743;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
 |||||
 DB 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 6
 ABL49283
 ID ABL49283 standard; cDNA; 1764 BP.
 XX
 AC ABL49283;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human lung tumour L523S recombinant polynucleotide SEQ ID NO:428.

DR P-PSDB; AABL1328.
 XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 PT in a patient -
 XX
 PS Claim 1a; Page 184-186; 261pp; English.
 XX
 CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 XX
 SQ Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
 Query Match 100.0%; Score 21; DB 21; Length 4181;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAAGTATCTTCAAGGAGCC 21
 Db 305 GAAAGTATCTTCAAGGAGCC 325
 RESULT 9
 ABL65405
 ID ABL65405 standard; DNA; 4181 BP.
 XX
 AC ABL65405;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Lung cancer related gene sequence SEQ ID NO:3742.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;
 KW cytostatic; Gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
 KW gene; ds.
 OS
 XX Homo sapiens.
 XX
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US10838.
 XX
 PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 22-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 25-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 26-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.

PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 02-OCT-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 03-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX
 PA (AVAL-) AVALON PHARM.
 XX
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 PI
 XX WPI; 2002-188264/24.
 XX
 XX Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 PS Claim 1; SEQ ID 3742; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.
 XX
 SQ Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
 Query Match 100.0%; Score 21; DB 24; Length 4181;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAAGTATCTTCAAGGAGCC 21
 Db 305 GAAAGTATCTTCAAGGAGCC 325
 RESULT 10
 ABL49119
 ID ABL49119 standard; cDNA; 4181 BP.
 XX
 AC ABL49119;
 XX
 DT 01-MAY-2002 (first entry)

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XX DE Human lung tumour L523S cDNA sequence SEQ ID NO:175.
 XX PN Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 KW immune response; ss.
 XX OS Homo sapiens.
 XX PN WO200200174-A2.
 XX PD 03-JAN-2002.
 XX PF 28-JUN-2001; 2001WO-US21065.
 XX PR 28-JUN-2000; 2000US-0606421.
 XX PR 02-AUG-2000; 2000US-0630940.
 XX PR 21-AUG-2000; 2000US-0643597.
 XX PR 15-SEP-2000; 2000US-0662786.
 XX PR 09-OCT-2000; 2000US-0685696.
 XX PR 12-DEC-2000; 2000US-0735705.
 XX PR 07-MAY-2001; 2001US-0850716.
 XX PA (CORI-) CORIXA CORP.
 XX PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
 XX WPI; 2002-090513/12.
 DR P-PSDB; ABB74960.
 XX Polynucleotides encoding lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 XX Example 2; Page 266-267; 374pp; English.
 XX The present invention describes human lung tumor proteins. Human lung
 CC tumor proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumor proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumor proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.
 XX Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
 SQ Query Match 100.0%; Score 21; DB 24; Length 4181;
 Best Local Similarity 100.0%; Pred. No. 0.63; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0;
 QY 1 GAAAGTATCTTCAAGGACGCC 21
 Db 305 GAAAGTATCTTCAAGGACGCC 325
 RESULT 11
 ABA99958
 ID ABA99958 standard; DNA; 4601 BP.
 XX AC ABA99958;
 XX 05-JUL-2002 (first entry)
 DT Human KOC DNA.
 DE KOC; promoter; human; cytostatic; dermatological; vulnary; tumour;
 KW chemotherapy; allogenic bone marrow transplant; pancreatic carcinoma;
 KW domain-containing protein overexpressed in cancer; immunostimulant;
 KW gene therapy; chronic pancreatitis; pluripotency; aging; wound healing;
 KW radiation therapy; skin regeneration; cell differentiation; cancer; ds.
 XX

OS Homo sapiens.
 XX PN WO200220036-A1.
 XX PD 14-MAR-2002.
 XX PF 01-AUG-2001; 2001WO-DE02948.
 XX PR 06-SEP-2000; 2000DE-1043964.
 XX PR 14-FEB-2001; 2001DE-1006829.
 XX PA (MUEL/) MUELLER F.
 XX PI Mueller F, Gress T, Adler G;
 XX WPI; 2002-292230/33.
 DR New promoter of the KOC gene, useful for diagnosis and treatment of
 PT cancer, for inducing cellular dedifferentiation and for identifying
 PT modulators -
 XX Claim 2; Fig 1a-b; 74pp; German.
 XX This invention describes a novel KOC (KH domain-containing protein
 CC overexpressed in cancer) promoter. The products of the invention have
 CC cytotatic, dermatological, vulnary and immunostimulant activity, are
 CC capable of modulating activity/expression of the KOC protein and can be
 CC used for gene therapy. The KOC promoter is also useful (i) for diagnosis
 CC of tumours that express KOC, particularly for differentiating between
 CC chronic pancreatitis and pancreatic carcinoma; (ii) to detect
 CC premalignant lesions of uncertain nature and to classify them for risk,
 CC and (iii) to evaluate treatments; (iv) to impart pluripotency to cells;
 CC (v) to prepare tissues or organs (by differentiation of stem cell
 CC populations); (vi) in high-dose chemotherapy; (vii) to improve ex vivo
 CC expansion of hematopoietic stem cells; (viii) to improve engraftment of
 CC allogenic bone marrow transplants; (ix) to slow down or reverse aging
 CC processes; (x) as prophylactic agents during chemotherapy/radiation
 CC therapy; (xi) to regenerate skin defects and accelerate wound healing,
 CC including for cosmetic purposes; and (xii) to immunise against malignant
 CC tumours or their precursor stages. The promoter can also be used (i) for
 CC isolation/enrichment/selective replication of stem cells; (ii) to
 CC determine the degree of (de)differentiation of cells and tissues; (iii)
 CC in gene therapy of cancer (for controlling protein expression); and (iv)
 CC to identify compounds, potentially useful in cancer treatment, that bind
 CC to the promoter and modulate its activity. The promoter makes possible
 CC generation of stem cells of any selected type. Since expression of KOC
 CC is not sensitive to other physiological states, e.g. inflammation, it
 CC represents a tumour marker with 100% sensitivity and specificity. This
 CC sequence represents the human KOC gene described in the disclosure of
 CC the invention.
 XX Sequence 4601 BP; 1462 A; 906 C; 918 G; 1298 T; 17 other;
 SQ Query Match 100.0%; Score 21; DB 24; Length 4601;
 Best Local Similarity 100.0%; Pred. No. 0.64; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0;
 QY 1 GAAAGTATCTTCAAGGACGCC 21
 Db 725 GAAAGTATCTTCAAGGACGCC 745
 RESULT 12
 AAS86150
 ID AAS86150 standard; cDNA; 4264 BP.
 XX AC AAS86150;
 XX 13-FEB-2002 (first entry)
 DT DNA encoding novel human diagnostic protein #21954.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW

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PF WO200250301-A2.
XX 27-JUN-2002.
XX 18-DEC-2001; 2001WO-US48276.
XX 18-DEC-2000; 2000US-255892P.
XX 24-APR-2001; 2001US-285691P.
XX (GENE-) GENE LOGIC INC.
XX (PROC ) PROCTER & GAMBLE CO.
XX Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
XX Mertz L;
XX WPI; 2002-557663/59.
XX
XX Use of genes and their expression profiles associated with osteoblast
XX differentiation for screening modulators bone formation, for diagnosing
XX or treating e.g. osteoporosis, or as markers for the differentiation
XX process -
XX
XX Claim 1; SEQ ID NO 128; 78pp + Sequence Listing; English.
XX
XX The invention relates to genes and their expression profiles are used
XX for: screening modulators of precursor stem cell differentiation into
XX osteoblasts, or bone tissue deposition;
XX (a) diagnosing abnormal deposition of bone tissue, abnormal rate of
XX osteoblast formation or osteoporosis; or
XX (c) treating or monitoring treatment of the conditions cited in (b), or
XX monitoring the progression of bone tissue deposition.
XX Specific conditions include postmenopausal osteoporosis, glucocorticoid
XX osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
XX drug-induced abnormalities in bone formation or bone loss, conditions
XX that involve altered bone metabolism (e.g. idiopathic juvenile
XX osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
XX Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
XX osteoblast differentiation associated cDNA marker of the invention.
XX Note: the sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 7661 BP; 1707 A; 1826 C; 1815 G; 2311 T; 2 other;
XX
XX Query Match 80.0%; Score 16.8; DB 24; Length 7661;
XX Best Local Similarity 90.0%; Pred. No. 1.1e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 AAGATATCTTCAAGGAGGCC 21
XX ||||| ||||| ||||| ||||| |||||
XX Db 2160 AAGATCTCTTCAAGGAGGCC 2141
XX
XX RESULT 15
XX ABL13727/c
XX ID ABL13727 standard; cDNA; 557 BP.
XX
XX AC ABL13727;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 35663.
XX
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
XX OS Drosophila melanogaster.
XX
XX FN WO200171042-A2.
XX
XX PD 27-SEP-2001.
XX
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX P-PSDB; ABB69624.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 35663; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABH57737-ABH72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 557 BP; 135 A; 126 C; 139 G; 157 T; 0 other;
XX
XX Query Match 78.1%; Score 16.4; DB 23; Length 557;
XX Best Local Similarity 94.4%; Pred. No. 1.1e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 4 AGTATCTTCAAGGAGGCC 21
XX ||||| ||||| ||||| ||||| |||||
XX Db 177 AGTATCTTCAAGGAGGCC 160
XX
XX Search completed: April 18, 2003, 05:45:16
XX Job time : 97.5455 secs

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:53:41 ; Search time 20.5227 Seconds
(without alignments)
313.809 Million cell updates/sec

Title: US-09-270-437d-9

Perfect score: 21
Sequence: 1 GAAAGTATCTTCAAGGAGGCC 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	1740	4	US-09-643-597-347
2	21	100.0	4159	4	US-09-061-709-4
3	21	100.0	4181	4	US-09-643-597-175
4	15.8	75.2	936	2	US-08-288-663A-13
5	15.8	75.2	1194	2	US-08-288-663A-2
6	15.8	75.2	1228	2	US-08-288-663A-3
7	15.4	73.3	3207	1	US-08-045-806-1
8	15.4	73.3	3207	1	US-08-366-051B-1
9	15.4	73.3	5261	1	US-08-045-806-3
10	15.4	73.3	5261	1	US-08-366-051B-3
11	15.2	72.4	579	4	US-09-026-601-29
12	15.2	72.4	579	4	US-09-026-601-30
13	15.2	72.4	579	4	US-09-026-601-31
14	15.2	72.4	579	4	US-09-026-601-32
15	15.2	72.4	579	4	US-09-026-601-34
16	15.2	72.4	579	4	US-09-026-601-36
17	15.2	72.4	579	4	US-09-026-601-33
18	15.2	72.4	580	4	US-09-026-601-35
19	15.2	72.4	580	4	US-09-026-601-37
20	15.2	72.4	580	4	US-09-026-601-39
21	15.2	72.4	4422	4	US-09-166-350-1
22	15.2	72.4	7207	4	US-09-462-606-3
23	14.8	70.5	580	4	US-09-026-601-40
24	14.8	70.5	642	4	US-08-998-416-1126
25	14.6	69.5	399	4	US-09-134-003C-1761
26	14.6	69.5	433	1	US-08-664-596B-1
27	14.6	69.5	433	1	US-08-738-367-1

ALIGNMENTS

RESULT 1

US-09-643-597-347
; Sequence 347, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Lihun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-347

Query Match 100.0%; Score 21; DB 4; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGAGGCC 21
|||||

Db 55 GAAAGTATCTTCAAGGAGGCC 75
|||||

RESULT 2

US-09-061-709-4
; Sequence 4, Application US/09061709B
; Patent No. 6297364
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.

Sequence 6, Appli
Sequence 84, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 39, Appli
Sequence 454, Appli
Sequence 2, Appli
Sequence 1, Appli

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen, The Antigens Per Se, And Uses Thereof

FILE REFERENCE: LUD 5538

CURRENT FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 4

LENGTH: 4159

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

US-09-061-709-4

Query Match 100.0%; Score 21; DB 4; Length 4159;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGAGCC 21

DB 305 GAAAGTATCTTCAAGGAGCC 325

RESULT 3

US-09-643-597-175

Sequence 175, Application US/09643597

Patent No. 6426072

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Kalos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C11

CURRENT FILING DATE: US/09/643,597

NUMBER OF SEQ ID NOS: 369

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 175

LENGTH: 4181

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure

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NAME/KEY: unsure

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NAME/KEY: unsure

LOCATION: (3940)

OTHER INFORMATION: n=A,T,C or G

NAME/KEY: unsure

LOCATION: (3940)

OTHER INFORMATION: n=A,T,C or G

NAME/KEY: unsure

LOCATION: (3940)

OTHER INFORMATION: n=A,T,C or G

REFERENCE/DOCKET NUMBER: 44612
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 936 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-288-663A-13

Query Match 75.2%; Score 15.8; DB 2; Length 936;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAAGTATCTTCAAGGACG 20
Db 781 ACAGTATCTTCAAGGAGC 799

RESULT 5
US-08-288-663A-2
Sequence 2, Application US/08288663A
Patent No. 5879896
GENERAL INFORMATION:
APPLICANT: HINUMA, Shuji
APPLICANT: HOSOYA, Masaki
TITLE OF INVENTION: HUMAN TRH RECEPTOR, ITS PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,663A
FILING DATE: 09-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 198309/1993
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: 286986/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 325215/1993
FILING DATE: 22-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44612
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-288-663A-2

Query Match 75.2%; Score 15.8; DB 2; Length 1194;
Best Local Similarity 89.5%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AAAGTATCTTCAAGGACG 20
Db 769 ACAGTATCTTCAAGGAGC 787

RESULT 6
US-08-288-663A-3
Sequence 3, Application US/08288663A
Patent No. 5879896
GENERAL INFORMATION:
APPLICANT: HINUMA, Shuji
APPLICANT: HOSOYA, Masaki
TITLE OF INVENTION: HUMAN TRH RECEPTOR, ITS PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,663A
FILING DATE: 09-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 198309/1993
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: 286986/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 325215/1993
FILING DATE: 22-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44612
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1228 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-288-663A-3

Query Match 75.2%; Score 15.8; DB 2; Length 1228;
Best Local Similarity 89.5%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAAGTATCTTCAAGGACG 20
Db 781 ACAGTATCTTCAAGGAGC 799

RESULT 7
US-08-045-806-1
Sequence 1, Application US/08045806
Patent No. 5378822

us-09-270-437d-9.rnl

Mon Apr 21 10:30:52 2003

```

;
; GENERAL INFORMATION:
; APPLICANT: Bradfield, Christopher Alan
; APPLICANT: Dolwick, Kristin Marie
; APPLICANT: Poland, Alan
; TITLE OF INVENTION: Ah Receptor cDNA and Method of
; TITLE OF INVENTION: Determining Human Risks To Environmental Pollutants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/045,806
; FILING DATE: 19930408
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pentress, Susan B.
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-9207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2415
; US-08-045-806-1
;
; Query Match 73.3%; Score 15.4; DB 1; Length 3207;
; Best Local Similarity 94.1%; Pred.No. 60;
; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 2 AAAGTATCTTCAAGGAC 18
Db 711 AAAGTATCTTCATGGAC 727

;
; RESULT 8
; US-08-366-051B-1
; Sequence 1, Application US/08366051B
; Patent No. 5650283
; GENERAL INFORMATION:
; APPLICANT: Bradfield, Christopher A.
; APPLICANT: Dolwick, Kristin M.
; APPLICANT: Carver, Lucy A.
; TITLE OF INVENTION: Ah Receptor cDNAs and Genetically
; TITLE OF INVENTION: Engineered Cells for Detecting Agonists to the Ah
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,051B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Tilton, Timothy L.
; REGISTRATION NUMBER: 16,926
; REFERENCE/DOCKET NUMBER: NU-9207-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2415
; US-08-366-051B-1
;
; Query Match 73.3%; Score 15.4; DB 1; Length 3207;
; Best Local Similarity 94.1%; Pred.No. 60;
; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 2 AAAGTATCTTCAAGGAC 18
Db 711 AAAGTATCTTCATGGAC 727

;
; RESULT 9
; US-08-045-806-3
; Sequence 3, Application US/08045806
; Patent No. 5378822
; GENERAL INFORMATION:
; APPLICANT: Bradfield, Christopher Alan
; APPLICANT: Dolwick, Kristin Marie
; APPLICANT: Poland, Alan
; TITLE OF INVENTION: Ah Receptor cDNA and Method of
; TITLE OF INVENTION: Determining Human Risks To Environmental Pollutants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/045,806
; FILING DATE: 19930408
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pentress, Susan B.
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: NU-9207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5261 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double

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;; TOPOLOGY: unknown
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 383..2927
US-08-045-806-3

Query Match 73.3%; Score 15.4; DB 1; Length 5261;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAAGTATCTTCAAGGAC 18
|||||
Db 1111 AAAGTATCTTCAAGGAC 1127

RESULT 10

US-08-366-051B-3
; Sequence 3, Application US/08366051B
; Patent No. 5650283

GENERAL INFORMATION:

;; APPLICANT: Bradfield, Christopher A.

;; APPLICANT: Dolwick, Kristin M.

;; APPLICANT: Carver, Lucy A.

;; TITLE OF INVENTION: Ah Receptor cDNAs and Genetically

;; TITLE OF INVENTION: Engineered Cells for Detecting Agonists to the Ah

;; NUMBER OF SEQUENCES: 36

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut

;; STREET: 100 South Wacker Drive, Suite 960

;; CITY: Chicago

;; STATE: Illinois

;; COUNTRY: USA

;; ZIP: 60606-4002

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/366,051B

;; FILING DATE:

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Tilton, Timothy L.

;; REGISTRATION NUMBER: 16,926

;; REFERENCE/DOCKET NUMBER: NU-9207-CIP

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (312)-456-8000

;; TELEFAX: (312)-456-7776

;; INFORMATION FOR SEQ ID NO: 3:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 5261 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: double

;; TOPOLOGY: unknown

;; MOLECULE TYPE: cDNA

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 383..2927

US-08-366-051B-3

Query Match 73.3%; Score 15.4; DB 1; Length 5261;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAAGTATCTTCAAGGAC 18
|||||

Db 1111 AAAGTATCTTCAAGGAC 1127

RESULT 11

US-09-026-601-29/c
; Sequence 29, Application US/09026601
; Patent No. 6358680

GENERAL INFORMATION:

;; APPLICANT: Beck, James J.

;; TITLE OF INVENTION: Detection of Wheat and Barley Fungal

;; TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction

;; NUMBER OF SEQUENCES: 41

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: No. 6358680artis Corporation

;; STREET: 3054 Cornwallis Road

;; CITY: Research Triangle Park

;; STATE: No. 6358680th Carolina

;; COUNTRY: USA

;; ZIP: 27709

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/026,601

;; FILING DATE:

;; CLASSIFICATION:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Meigs, J. Timothy

;; REGISTRATION NUMBER: 38,241

;; REFERENCE/DOCKET NUMBER: CGC 1984

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 919-541-8587

;; TELEFAX: 919-541-8689

;; INFORMATION FOR SEQ ID NO: 29:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 579 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)

;; ORIGINAL SOURCE:

;; ORGANISM: Pyrenophora tritici-repentis

;; INDIVIDUAL ISOLATE: consensus sequence

;; FEATURE:

;; NAME/KEY: misc feature

;; LOCATION: 1..30

;; OTHER INFORMATION: /note= "3' end of small subunit

;; OTHER INFORMATION: rRNA gene"

;; FEATURE:

;; NAME/KEY: misc feature

;; LOCATION: 31..208

;; OTHER INFORMATION: /note= "ITS1"

;; FEATURE:

;; NAME/KEY: misc feature

;; LOCATION: 209..365

;; OTHER INFORMATION: /note= "5.8S rRNA gene"

;; FEATURE:

;; NAME/KEY: misc feature

;; LOCATION: 366..526

;; OTHER INFORMATION: /note= "ITS2"

;; FEATURE:

;; NAME/KEY: misc feature

;; LOCATION: 527..579

;; OTHER INFORMATION: /note= "5' end of large subunit

;; OTHER INFORMATION: rRNA gene"

US-09-026-601-29

Query Match 72.4%; Score 15.2; DB 4; Length 579;
Best Local Similarity 85.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGACG 20
|||||

Db 515 GAAAGTATCTTCAAGGACG 496
|||||

us-09-270-437d-9.rni

Mon Apr 21 10:30:52 2003

QY 1 GAAAGTATCTTCAAGGACGC 20
 Db 515 GAAAGAAGCTTCATGGACGC 496
 RESULT 13
 US-09-026-601-31/c
 ; Sequence 31, Application US/09026601
 ; Patent No. 6358680
 ; GENERAL INFORMATION:
 ; APPLICANT: Beck, James J.
 ; TITLE OF INVENTION: Detection of Wheat and Barley Fungal
 ; TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
 ; NUMBER OF SEQUENCES: 41
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6358680artis Corporation
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: No. 6358680th Carolina
 ; COUNTRY: USA
 ; ZIP: 27709
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/026,601
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meigs, J. Timothy
 ; REGISTRATION NUMBER: 38,241
 ; REFERENCE/DOCKET NUMBER: CGC 1984
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-541-8587
 ; TELEFAX: 919-541-8689
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 579 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; ORGANISM: Pyrenophora tritici-repentis
 ; IMMEDIATE SOURCE:
 ; INDIVIDUAL ISOLATE: 119-2-3
 ; CLONE: 2-2
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..30
 ; OTHER INFORMATION: /note= "3' end of small subunit
 ; OTHER INFORMATION: rRNA gene"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 31..208
 ; OTHER INFORMATION: /note= "ITS1"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 209..365
 ; OTHER INFORMATION: /note= "5.8S rRNA gene"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 366..526
 ; OTHER INFORMATION: /note= "ITS2"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 527..579
 ; OTHER INFORMATION: /note= "5' end of large subunit
 ; OTHER INFORMATION: rRNA gene"
 ; US-09-026-601-31

RESULT 12
 US-09-026-601-30/c
 ; Sequence 30, Application US/09026601
 ; Patent No. 6358680
 ; GENERAL INFORMATION:
 ; APPLICANT: Beck, James J.
 ; TITLE OF INVENTION: Detection of Wheat and Barley Fungal
 ; TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
 ; NUMBER OF SEQUENCES: 41
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6358680artis Corporation
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: No. 6358680th Carolina
 ; COUNTRY: USA
 ; ZIP: 27709
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/026,601
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meigs, J. Timothy
 ; REGISTRATION NUMBER: 38,241
 ; REFERENCE/DOCKET NUMBER: CGC 1984
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-541-8587
 ; TELEFAX: 919-541-8689
 ; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 579 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; ORGANISM: Pyrenophora tritici-repentis
 ; IMMEDIATE SOURCE:
 ; INDIVIDUAL ISOLATE: 6715
 ; CLONE: 2 and 4 (consensus)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..30
 ; OTHER INFORMATION: /note= "3' end of small subunit
 ; OTHER INFORMATION: rRNA gene"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 31..208
 ; OTHER INFORMATION: /note= "ITS1"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 209..365
 ; OTHER INFORMATION: /note= "5.8S rRNA gene"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 366..526
 ; OTHER INFORMATION: /note= "ITS2"
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 527..579
 ; OTHER INFORMATION: /note= "5' end of large subunit
 ; OTHER INFORMATION: rRNA gene"
 ; US-09-026-601-30
 Query Match 72.4%; Score 15.2; DB 4; Length 579;
 Best Local Similarity 85.0%; Pred. No. 54;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Query Match          72.4%; Score 15.2; DB 4; Length 579;
Best Local Similarity 85.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGC 20
    ||||| ||||| |||||
Db 515 GAAAGAAGCTTCATGACGC 496

RESULT 14
US-09-026-601-32/c
; Sequence 32, Application US/09026601
; Patent No. 6358680
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: Detection of Wheat and Barley Fungal
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6358680artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6358680th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026.601
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1984
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Pyrenophora tritici-repentis
; INDIVIDUAL ISOLATE: DL22
; IMMEDIATE SOURCE:
; CLONE: 1-1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31..208
; OTHER INFORMATION: /note= "ITS1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 209..365
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 366..526
; OTHER INFORMATION: /note= "ITS2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 527..579

Query Match          72.4%; Score 15.2; DB 4; Length 579;
Best Local Similarity 85.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGC 20
    ||||| ||||| |||||
Db 515 GAAAGAAGCTTCATGACGC 496

RESULT 15
US-09-026-601-34/c
; Sequence 34, Application US/09026601
; Patent No. 6358680
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: Detection of Wheat and Barley Fungal
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6358680artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6358680th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026.601
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1984
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Pyrenophora tritici-repentis
; INDIVIDUAL ISOLATE: 44184
; IMMEDIATE SOURCE:
; CLONE: 3-1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /note= "3' end of small subunit"
; OTHER INFORMATION: rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31..208
; OTHER INFORMATION: /note= "ITS1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 209..365
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 366..526
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Mon Apr 21 10:30:52 2003

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; OTHER INFORMATION: /note= "ITS2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 527..579
; OTHER INFORMATION: /note= "5' end of large subunit
; OTHER INFORMATION: rRNA gene"
; US-09-026-601-34
Query Match      72.4%; Score 15.2; DB 4; Length 579;
Best Local Similarity 85.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAAGTATCTTCAGGACGC 20
   ||||| ||||| ||||| |||||
Db 515 GAAAGACCTTCAGGACGC 496

Search completed: April 18, 2003, 07:34:12
Job time : 25.5227 secs

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GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 06:35:31 ; Search time 87.1818 Seconds
(without alignments)
241.975 Million cell updates/sec

Title: US-09-270-437D-9

Perfect score: 21
Sequence: 1 gaaagtattctcaaggagcc 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 639749 seqs, 502280978 residues

Total number of hits satisfying chosen parameters: 1279498

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	1740	10	US-09-735-705-347
2	21	100.0	1740	10	US-09-850-716A-347
3	21	100.0	1740	10	US-09-897-778-347
4	21	100.0	1743	10	US-09-897-778-447
5	21	100.0	1743	10	US-09-897-778-450
6	21	100.0	1764	10	US-09-850-716A-428
7	21	100.0	1764	10	US-09-897-778-428
8	21	100.0	4159	10	US-09-899-651-4
9	21	100.0	4181	10	US-09-735-705-175
10	21	100.0	4181	10	US-09-954-456-715
11	21	100.0	4181	10	US-09-850-716A-175
12	21	100.0	4181	10	US-09-897-778-175
13	16.2	77.1	359	10	US-09-897-778-175
14	16.2	77.1	476	10	US-09-864-761-23958
15	16.2	77.1	479	10	US-09-864-761-1856
16	16.2	77.1	479	10	US-09-880-107-2877
17	16.2	77.1	597	10	US-09-864-761-7227
18	16.2	77.1	1178	10	US-09-925-300-662
19	16.2	77.1	9862	9	US-09-764-872-797
	15.8	75.2	32191	10	US-09-764-864-1678

c	20	15.8	75.2	1691139	9	US-10-067-514-1	Sequence 1, Appli
	21	15.4	73.3	533	10	US-09-867-701-4800	Sequence 4800, Ap
	22	15.4	73.3	626	10	US-09-770-149-734	Sequence 734, App
	23	15.4	73.3	3555	12	US-10-044-090-527	Sequence 527, App
	24	15.4	73.3	5866	12	US-10-044-090-215	Sequence 215, App
	25	15.2	72.4	1686	10	US-09-731-872-183	Sequence 183, App
	26	15.2	72.4	3468	9	US-10-042-141-36	Sequence 36, Appl
	27	15.2	72.4	22161	9	US-09-726-643-36	Sequence 36, Appl
	28	15.2	72.4	22161	9	US-10-092-154-1020	Sequence 1020, Ap
	29	15.2	72.4	106323	10	US-09-764-847-1020	Sequence 1020, Ap
	30	15.2	72.4	536165	9	US-09-803-661-3	Sequence 3, Appli
	31	15.2	72.4	536165	9	US-09-939-964-1	Sequence 1, Appli
	32	15	71.4	373	9	US-09-933-797-113	Sequence 113, App
	33	14.8	70.5	167	10	US-09-728-445-394	Sequence 394, App
	34	14.8	70.5	275	10	US-09-783-590-3645	Sequence 3645, Ap
	35	14.8	70.5	465	10	US-09-864-761-1651	Sequence 1651, Ap
	36	14.8	70.5	487	10	US-09-864-761-2009	Sequence 2009, Ap
	37	14.8	70.5	501	10	US-09-998-598-802	Sequence 802, App
	38	14.8	70.5	549	10	US-09-864-761-9819	Sequence 9819, Ap
	39	14.8	70.5	601	10	US-09-920-300A-908	Sequence 908, App
	40	14.8	70.5	601	12	US-10-033-528-908	Sequence 908, App
	41	14.8	70.5	1074	9	US-09-938-842A-2656	Sequence 2656, Ap
	42	14.8	70.5	3180	10	US-09-949-192-14	Sequence 14, Appl
	43	14.8	70.5	4322	9	US-10-098-841-252	Sequence 252, App
	44	14.8	70.5	18355	7	US-08-781-986A-67	Sequence 67, Appl
	45	14.8	70.5	20029	9	US-10-092-154-1624	Sequence 1624, Ap

ALIGNMENTS

RESULT 1

US-09-735-705-347

Sequence 347, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Pan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
TYPE: DNA
ORGANISM: Homo sapiens
US-09-735-705-347

Query Match 100.0%; Score 21; DB 10; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.28; 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 GAAAGTATCTTCAAGGAGCC 21

Db 55 GAAAGTATCTTCAAGGAGCC 75

RESULT 2

US-09-850-716A-347
Sequence 347, Application US/09850716A

us-09-270-437d-9.rnpb

Mon Apr 21 10:30:54 2003

```

; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-850-716A-347

Query Match      100.0%; Score 21; DB 10; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGAGCC 21
   |||||
Db 55 GAAAGTATCTTCAAGGAGCC 75

RESULT 3
US-09-897-778-347
; Sequence 347, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-897-778-347

Query Match      100.0%; Score 21; DB 10; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGAGCC 21
   |||||
Db 55 GAAAGTATCTTCAAGGAGCC 75

RESULT 4
US-09-897-778-447
; Sequence 447, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-897-778-447

Query Match      100.0%; Score 21; DB 10; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGAGCC 21
   |||||
Db 55 GAAAGTATCTTCAAGGAGCC 75

RESULT 5
US-09-897-778-450
; Sequence 450, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 450
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-897-778-450

Query Match      100.0%; Score 21; DB 10; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGAGCC 21
   |||||
Db 55 GAAAGTATCTTCAAGGAGCC 75

RESULT 6
US-09-850-716A-428
; Sequence 428, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; APPLICANT: Carter, Darrick

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; CURRENT APPLICATION NUMBER: US/09/850,716A
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 428
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-850-716A-428

Query Match 100.0%; Score 21; DB 10; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0.28; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
| | | | | | | | | | | | | | | | | | | | | |
DB 76 GAAAGTATCTTCAAGGACGCC 96

RESULT 7

US-09-897-778-428
; Sequence 428, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 428
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-428

Query Match 100.0%; Score 21; DB 10; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0.28; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
| | | | | | | | | | | | | | | | | | | | | |
DB 76 GAAAGTATCTTCAAGGACGCC 96

RESULT 8

US-09-899-651-4
; Sequence 4, Application US/09899651
; Patent No. US20020111470A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; FILE REFERENCE: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06

; PRIOR APPLICATION NUMBER: US/09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 4
; LENGTH: 4159
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-4

Query Match 100.0%; Score 21; DB 10; Length 4159;
Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
| | | | | | | | | | | | | | | | | | | | | |
DB 305 GAAAGTATCTTCAAGGACGCC 325

RESULT 9

US-09-735-705-175
; Sequence 175, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3347)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (3502)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (3506)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (3520)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (3538)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (3549)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (3646)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (3940)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure

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LOCATION: (3968)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3974)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4036)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4056)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4062)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4080)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4088)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4115)
OTHER INFORMATION: n=A,T,C or G
US-09-735-705-175

Query Match          100.0%; Score 21; DB 10; Length 4181;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAAAGTATCTTCAAGGAGCC 21
        |||||
DB      305 GAAAGTATCTTCAAGGAGCC 325

RESULT 10
US-09-954-456-715
; Sequence 715, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 715
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature

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OTHER INFORMATION: n=A,T,C or G
 NAME/KEY: unsure
 LOCATION: (4088)
 OTHER INFORMATION: n=A,T,C or G
 NAME/KEY: unsure
 LOCATION: (4115)
 OTHER INFORMATION: n=A,T,C or G
 US-09-850-716A-175

Query Match 100.0%; Score 21; DB 10; Length 4181;
 Best Local Similarity 100.0%; Pred. No. 0.32; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0;

Qy 1 GAAAGTATCTTCAAGGACGCC 21
 |||||
 Db 305 GAAAGTATCTTCAAGGACGCC 325

RESULT 12

US-09-897-778-175
 Sequence 175, Application US/09897778
 Patent No. US20020147143A1

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
 APPLICANT: Marnerakis, Margarita
 APPLICANT: Fanger, Gary R.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Watanabe, Yoshihiro
 APPLICANT: Henderson, Robert A.
 APPLICANT: Peckham, David W.
 APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C16

CURRENT APPLICATION NUMBER: US/09/897,778

NUMBER OF SEQ ID NOS: 467

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 175

LENGTH: 4181

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 3347, 3502, 3506, 3520, 3538, 3549, 3646, 3940, 3968, 3974,

LOCATION: 4036, 4056, 4062, 4080, 4088, 4115

OTHER INFORMATION: n = A,T,C or G

US-09-897-778-175

Query Match 100.0%; Score 21; DB 10; Length 4181;
 Best Local Similarity 100.0%; Pred. No. 0.32; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0;

Qy 1 GAAAGTATCTTCAAGGACGCC 21
 |||||
 Db 305 GAAAGTATCTTCAAGGACGCC 325

RESULT 13

US-09-864-761-23958/c

Sequence 23958, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeonica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 23958
 LENGTH: 359
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL121777.16
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
 OTHER INFORMATION: NT HIT: gi4507208, EVALUE 1.00e-15
 OTHER INFORMATION: SWISSPROT HIT: P19623, EVALUE 2.00e-14
 OTHER INFORMATION: EST_HUMAN HIT: BE904452.1, EVALUE 2.00e-15
 US-09-864-761-23958

Query Match 77.1%; Score 16.2; DB 10; Length 359;
 Best Local Similarity 85.7%; Pred. No. 65;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGACGCC 21
 |||||
 Db 279 GAAAGCTCTTCAAGGACGCC 259

RESULT 14

US-09-864-761-1856

Sequence 1856, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1856
LENGTH: 476
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO Z95330.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
US-09-864-761-1856

Query Match	77.1%	Score 16.2;	DB 10;	Length 476;
Best Local Similarity	85.7%	Pred. No. 68;		
Matches 18;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	GAAGAATATCTTCAAGGAGCC	21	
Db	428	GAAGGCCTCTTCAAGGAGCC	448	

RESULT 15

```

US-09-880-107-2877
; Sequence 2877, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2877
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 R49047
US-09-880-107-2877

Query Match 77.1%; Score 16.2; DB 10; Length 479;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches 3; Indels 0;

QY 1 GAAAGTATCTTCAGGAGGCC 21
DB 223 GAAAGGAACTTCAGGAGGCC 243

Search completed: April 18, 2003, 10:13:04
Job time : 92.3485 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	21	100.0	422	16	US-09-271	490-1301	Sequence 1
2	21	100.0	432	34	US-09-925	552-13091	Sequence 1
3	21	100.0	432	38	US-10-038	354-13091	Sequence 1
4	21	100.0	438	16	US-09-287	618-27259	Sequence 1
5	21	100.0	529	17	US-09-399	932-638	Sequence 1
6	21	100.0	556	25	US-09-652	133-4489	Sequence 1
7	21	100.0	834	25	US-09-652	123-8442	Sequence 1
8	21	100.0	843	17	US-09-399	932-4493	Sequence 1
9	21	100.0	1740	1	PCF-US01	47576-347	Sequence 3
10	21	100.0	1740	21	US-09-542	615A-347	Sequence 1
11	21	100.0	1740	23	US-09-606	421A-347	Sequence 1
12	21	100.0	1740	23	US-09-606	421B-347	Sequence 1
13	21	100.0	1740	24	US-09-630	940A-347	Sequence 1
14	21	100.0	1740	24	US-09-630	940B-347	Sequence 1
15	21	100.0	1740	26	US-09-662	786-347	Sequence 1
16	21	100.0	1740	27	US-09-685	696-347	Sequence 1
17	21	100.0	1740	29	US-09-735	705-347	Sequence 1
18	21	100.0	1740	32	US-09-850	716-347	Sequence 1
19	21	100.0	1740	32	US-09-850	716A-347	Sequence 1
20	21	100.0	1740	33	US-09-897	778-347	Sequence 1
21	21	100.0	1740	38	US-10-007	700-347	Sequence 1

22	21	100.0	1740	40	US-10-117-982-347	Sequence 347, App
23	21	100.0	1740	40	US-10-117-982-478	Sequence 478, App
24	21	100.0	1740	40	US-10-117-982-483	Sequence 483, App
25	21	100.0	1743	1	PCT-US01-47576-447	Sequence 447, App
26	21	100.0	1743	1	PCT-US01-47576-450	Sequence 450, App
27	21	100.0	1743	33	US-09-897-778-447	Sequence 447, App
28	21	100.0	1743	33	US-09-897-778-450	Sequence 450, App
29	21	100.0	1743	38	US-10-007-700-447	Sequence 447, App
30	21	100.0	1743	38	US-10-007-700-450	Sequence 450, App
31	21	100.0	1743	40	US-10-117-982-447	Sequence 447, App
32	21	100.0	1743	40	US-10-117-982-450	Sequence 450, App
33	21	100.0	1764	1	PCT-US01-47576-428	Sequence 428, App
34	21	100.0	1764	32	US-09-850-716-428	Sequence 428, App
35	21	100.0	1764	32	US-09-850-716A-428	Sequence 428, App
36	21	100.0	1764	33	US-09-897-778-428	Sequence 428, App
37	21	100.0	1764	38	US-10-007-700-428	Sequence 428, App
38	21	100.0	1764	40	US-10-117-982-428	Sequence 428, App
39	21	100.0	4159	16	US-09-270-437-4	Sequence 4, Appli
40	21	100.0	4159	33	US-09-899-651-4	Sequence 4, Appli
41	21	100.0	4181	1	PCT-US01-47576-175	Sequence 175, App
42	21	100.0	4181	18	US-09-466-396A-175	Sequence 175, App
43	21	100.0	4181	18	US-09-476-496A-175	Sequence 175, App
44	21	100.0	4181	19	US-09-480-884A-175	Sequence 175, App
45	21	100.0	4181	19	US-09-510-376A-175	Sequence 175, App

ALIGNMENTS

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RESULT 1
US-09-271-490-13091
; Sequence 13091, Application US/09271490
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-767
; CURRENT APPLICATION NUMBER: US/09/271,490
; CURRENT FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 19424
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13091
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(422)
; OTHER INFORMATION: n = A,T,C or G
; US-09-271-490-13091

```

Query Match	100.0%;	Score 21;	DB 16;	Length 422;
Best Local Similarity	100.0%;	Pred. NO. 3.9;		
		Mismatches	0.	Indels 0;
		Gaps	0.	Gaps 0;

QY 1 GAAGTATCTTCAAGGACGC 21
|||||
Dh 369 GAAGTATCTTCAAGGACGC 389

RESULT 2
US-09-925-552-13091
; Sequence 13091, Application US/09925552
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-767
; CURRENT APPLICATION NUMBER: US/09/925,552
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/271,490
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 19424

```

; SOFTWARE: FastSeq for Windows Version 3.0
;
; SEQ ID NO 13091
;
; LENGTH: 422
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: misc_feature
;
; LOCATION: (1)...(422)
;
; OTHER INFORMATION: n = A,T,C or G
US-09-925-552-13091

```

```
Query Match      100.0%; Score 21; DB 34; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||
Db 369 GAAAGTATCTTCAAGGACGCC 389

```

RESULT 3
US-10-032-354-13091
; Sequence 13091, Application US/10032354
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-767
; CURRENT APPLICATION NUMBER: US/10/032,354
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/271,490
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 19424
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13091
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(422)
; OTHER INFORMATION: n = A,T,C or G
US-10-032-354-13091

```

```
Query Match      100.0%; Score 21; DB 38; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GAAAGTATCTTCAAGGACGCC 21
|||
nb 369 GAAAGTATCTTCAAGGACGCC 389

```

RESULT 4
US-09-287-618-27259
; Sequence 27259, Application US/09287618
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-768
; CURRENT APPLICATION NUMBER: US/09/287,618
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 27259
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-287-618-27259

```

Query Match	100.0%;	Score 21;	DB 16;	Length 438;
Best Local Similarity	100.0%;	Pred. No. 3.9;		

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
Db 388 GAAAGTATCTTCAAGGACGCC 408

RESULT 5

US-09-399-932-638
; Sequence 638, Application US/093999932
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: HUMAN BURKITT'S LYMPHOMA LIBRARY
; CURRENT APPLICATION NUMBER: US/09/399,932
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,464
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101,670
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106,456
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/126,902
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/132,067
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/144,447
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 5743
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 638
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(529)
; OTHER INFORMATION: n = A,T,C or G
US-09-399-932-638

Query Match 100.0%; Score 21; DB 17; Length 529;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
Db 94 GAAAGTATCTTCAAGGACGCC 114

RESULT 6

US-09-652-123-4489
; Sequence 4489, Application US/09652123
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: HUMAN BURKITT'S LYMPHOMA LIBRARY
; CURRENT APPLICATION NUMBER: US/09/652,123
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,464
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101,670
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106,456
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/126,902
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/132,067
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/144,447
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 5743
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4489
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(556)
; OTHER INFORMATION: n = A,T,C or G

US-09-652-123-4489

Query Match 100.0%; Score 21; DB 25; Length 556;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
Db 409 GAAAGTATCTTCAAGGACGCC 429

RESULT 7

US-09-652-123-8442
; Sequence 8442, Application US/09652123
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: HUMAN BURKITT'S LYMPHOMA LIBRARY
; CURRENT APPLICATION NUMBER: US/09/652,123
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,464
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101,670
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106,456
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/126,902
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/132,067
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/144,447
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 5743
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 842
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(834)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-123-8442

Query Match 100.0%; Score 21; DB 25; Length 834;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
Db 407 GAAAGTATCTTCAAGGACGCC 427

RESULT 8

US-09-399-932-4493
; Sequence 4493, Application US/093999932
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: HUMAN BURKITT'S LYMPHOMA LIBRARY
; CURRENT APPLICATION NUMBER: US/09/399,932
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,464
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101,670
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106,456
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/126,902
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/132,067
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/144,447
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 5743
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4493
; LENGTH: 843
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-399-932-4493

Query Match 100.0%; Score 21; DB 17; Length 843;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
DB 388 GAAAGTATCTTCAAGGACGCC 408

RESULT 9

PCT-US01-47576-347

; Sequence 347, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45503PC
; CURRENT APPLICATION NUMBER: PCT/US01/47576
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-47576-347

Query Match 100.0%; Score 21; DB 1; Length 1740;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
DB 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 10

US-09-542-615A-347

; Sequence 347, Application US/09542615A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347

; LENGTH: 1740

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-542-615A-347

Query Match 100.0%; Score 21; DB 21; Length 1740;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
DB 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 11

US-09-606-421A-347

; Sequence 347, Application US/09606421A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421A-347

Query Match 100.0%; Score 21; DB 23; Length 1740;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
DB 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 12

US-09-606-421B-347

; Sequence 347, Application US/09606421B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-606-421B-347

Query Match 100.0%; Score 21; DB 23; Length 1740;
Best Local Similarity 100.0%; Pred. No. 5.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 GAAAGTATCTTCAAGGACGCC 21
Db 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 13

US-09-630-940A-347
Sequence 347, Application US/09630940A

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C10
CURRENT APPLICATION NUMBER: US/09/630,940A
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
TYPE: DNA
ORGANISM: Homo sapiens

US-09-630-940A-347

Query Match 100.0%; Score 21; DB 24; Length 1740;
Best Local Similarity 100.0%; Pred. No. 5.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 GAAAGTATCTTCAAGGACGCC 21
Db 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 14

US-09-630-940B-347
Sequence 347, Application US/09630940B

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C10
CURRENT APPLICATION NUMBER: US/09/630,940B
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
TYPE: DNA

ORGANISM: Homo sapiens
US-09-630-940B-347

Query Match 100.0%; Score 21; DB 24; Length 1740;
Best Local Similarity 100.0%; Pred. No. 5.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 GAAAGTATCTTCAAGGACGCC 21
Db 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 15

US-09-662-786-347
Sequence 347, Application US/09662786

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C12
CURRENT APPLICATION NUMBER: US/09/662,786
CURRENT FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
TYPE: DNA
ORGANISM: Homo sapiens

US-09-662-786-347

Query Match 100.0%; Score 21; DB 26; Length 1740;
Best Local Similarity 100.0%; Pred. No. 5.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 GAAAGTATCTTCAAGGACGCC 21
Db 55 GAAAGTATCTTCAAGGACGCC 75

Search completed: April 18, 2003, 09:35:40
Job time : 1159.95 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:28 ; Search time 234.023 Seconds
(without alignments)
400.770 Million cell updates/sec

Title: US-09-270-437D-9

Perfect score: 21
Sequence: 1 gaaagtattctcaaggagcc 21

Scoring table: IDENTITY_NUC
Gapex 10.0 , Gapext 1.0

Searched: 5897297 seqs, 223308081 residues

Total number of hits satisfying chosen parameters: 11794594

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New:

1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3.*
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9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
10: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	5	US-09-270-437D-9
2	21	100.0	861	6	US-09-724-676-44306
3	21	100.0	861	6	US-09-724-676A-44306
4	21	100.0	1558	8	US-10-170-235-4888
5	21	100.0	1740	9	US-10-313-986-347
6	21	100.0	1740	9	US-10-313-986-478
7	21	100.0	1740	9	US-10-313-986-483
8	21	100.0	1743	9	US-10-313-986-447
9	21	100.0	1743	9	US-10-313-986-450
10	21	100.0	1764	9	US-10-313-986-428
11	21	100.0	1789	9	US-10-313-986-485
12	21	100.0	2137	6	US-09-724-676-44307
13	21	100.0	2137	6	US-09-724-676A-44307
14	21	100.0	4060	6	US-09-724-676-44305
15	21	100.0	4060	6	US-09-724-676A-44305
16	21	100.0	4159	5	US-09-270-437D-4
17	21	100.0	4181	9	US-10-313-986-175
18	21	100.0	4181	9	US-10-313-986-119-55
19	21	100.0	34555	9	US-10-313-986-479
20	19	90.5	201	11	US-60-453-135-15387
21	19	90.5	201	11	US-60-453-050-15387
22	19	90.5	3730	11	US-60-453-135-1

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23      19      90.5      3730      11      US-60-453-050-1      Sequence 1, Appli
24      18.4      87.6      1748      9      US-10-144-771-21075      Sequence 21075, A
25      17.4      82.9      25      11      US-60-427-808-455974      Sequence 455974, A
26      17.4      82.9      25      11      US-60-427-808-455975      Sequence 455975, A
27      16.8      80.0      268      6      US-09-532-315B-13848      Sequence 13848, A
28      16.8      80.0      414      7      US-09-675-784A-4706      Sequence 4706, Ap
29      16.8      80.0      7681      9      US-10-144-771-11275      Sequence 11275, A
30      16.2      77.1      123      6      US-09-532-315B-9552      Sequence 9552, Ap
31      16.2      77.1      201      11      US-60-453-680-84031      Sequence 84031, A
32      16.2      77.1      201      11      US-60-453-135-55791      Sequence 55791, A
33      16.2      77.1      201      11      US-60-453-050-55791      Sequence 55791, A
34      16.2      77.1      220      9      US-10-349-781-19519      Sequence 19519, A
35      16.2      77.1      254      6      US-09-532-315B-13854      Sequence 13854, A
36      16.2      77.1      272      6      US-09-532-315B-9553      Sequence 9553, Ap
37      16.2      77.1      300      9      US-10-144-771-39459      Sequence 39459, A
38      16.2      77.1      325      6      US-09-532-315B-9544      Sequence 9544, Ap
39      16.2      77.1      476      9      US-10-203-138A-1905      Sequence 1905, Ap
40      16.2      77.1      479      8      US-10-401-223-7878      Sequence 7878, Ap
41      16.2      77.1      538      6      US-09-532-315B-9551      Sequence 9551, Ap
42      16.2      77.1      544      6      US-09-532-315B-9556      Sequence 9556, Ap
43      16.2      77.1      568      6      US-09-532-315B-9555      Sequence 9555, Ap
44      16.2      77.1      601      7      US-09-947-907-19977      Sequence 19977, A
45      16.2      77.1

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ALIGNMENTS

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RESULT 1
US-09-270-437D-9
; Sequence 9, Application US/09270437D
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseung
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen
; TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538.1
; CURRENT APPLICATION NUMBER: US/09/270,437D
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 9
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-270-437D-9

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Query Match      100.0%; Score 21; DB 5; Length 21;
Beat Local Similarity 100.0%; Pred. No. 0.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAAAGTATCTTCAAGGAGGCC 21
DB 1 GAAAGTATCTTCAAGGAGGCC 21

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RESULT 2
US-09-724-676-44306
; Sequence 44306, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222

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Mon Apr 21 10:30:57 2003

us-09-270-437d-9.rnpn

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44306
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-44306

Query Match      100.0%; Score 21; DB 6; Length 861;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
   |||||
Db 321 GAAAGTATCTTCAAGGACGCC 341

RESULT 3
US-09-724-676A-44306
; Sequence 44306, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44306
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-44306

Query Match      100.0%; Score 21; DB 6; Length 861;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
   |||||
Db 321 GAAAGTATCTTCAAGGACGCC 341

RESULT 4
US-10-170-235-4888
; Sequence 4888, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 4888
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-4888

Query Match      100.0%; Score 21; DB 8; Length 1558;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
   |||||
Db 61 GAAAGTATCTTCAAGGACGCC 81

RESULT 5
US-10-313-986-347
; Sequence 347, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
US-10-313-986-347

Query Match      100.0%; Score 21; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
   |||||
Db 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 6
US-10-313-986-478
; Sequence 478, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-478

Query Match      100.0%; Score 21; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
   |||||
Db 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 7
US-10-313-986-483
; Sequence 483, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
US-10-313-986-483

Query Match      100.0%; Score 21; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
   |||||
Db 55 GAAAGTATCTTCAAGGACGCC 75

```

; SEQ ID NO 483
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: primate
US-10-313-986-483

Query Match 100.0%; Score 21; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
Db 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 8

US-10-313-986-447
; Sequence 447, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-447

Query Match 100.0%; Score 21; DB 9; Length 1743;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
Db 55 GAAAGTATCTTCAAGGACGCC 75

RESULT 9

US-10-313-986-450
; Sequence 450, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 450
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-450

Query Match 100.0%; Score 21; DB 9; Length 1743;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21

Db 55 GAAAGTATCTTCAAGGACGCC 75
|||||

RESULT 10

US-10-313-986-428
; Sequence 428, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 428
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-428

Query Match 100.0%; Score 21; DB 9; Length 1764;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
Db 76 GAAAGTATCTTCAAGGACGCC 96

RESULT 11

US-10-313-986-485
; Sequence 485, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 485
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-485

Query Match 100.0%; Score 21; DB 9; Length 1799;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
Db 74 GAAAGTATCTTCAAGGACGCC 94

RESULT 12

US-09-724-676-44307
; Sequence 44307, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen

Mon Apr 21 10:30:57 2003

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; Sequence 44305, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44305
; LENGTH: 4060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-44305

Query Match      100.0%; Score 21; DB 6; Length 4060;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGAGCGCC 21
   ||||||||||||||||||||
DB 321 GAAAGTATCTTCAAGGAGCGCC 341

Search completed: April 18, 2003, 10:03:36
Job time : 238.023 secs
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; Sequence 44305, Application US/09724,676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44307
; LENGTH: 2137
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-44307
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Query Match      100.0%; Score 21; DB 6; Length 2137;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGAGCGCC 21
   ||||||||||||||||||
DB 321 GAAAGTATCTTCAAGGAGCGCC 341
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RESULT 13
US-09-724-676A-44307
; Sequence 44307, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44307
; LENGTH: 2137
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-44307
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Query Match      100.0%; Score 21; DB 6; Length 2137;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGAGCGCC 21
   ||||||||||||||||||
DB 321 GAAAGTATCTTCAAGGAGCGCC 341
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RESULT 14
US-09-724-676-44305
; Sequence 44305, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44305
; LENGTH: 4060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-44305
```

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Query Match      100.0%; Score 21; DB 6; Length 4060;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGAGCGCC 21
   ||||||||||||||||||
DB 321 GAAAGTATCTTCAAGGAGCGCC 341
```

```
RESULT 15
US-09-724-676A-44305
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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:47:40 ; Search time 731.182 Seconds
(without alignments)
465.145 Million cell updates/sec

Title: US-09-270-437D-9

Perfect score: 21
Sequence: 1 gaagatatttcaggagcgc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estm:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	gb_gss:*
18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pln:*
21:	em_gss_vrt:*
22:	em_gss_fun:*
23:	em_gss_mam:*
24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
27:	em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	21	100.0	360	10	BE560346
2	21	100.0	361	10	BE269531
3	21	100.0	361	10	BE560268
4	21	100.0	366	10	BE396918
5	21	100.0	371	10	BE560799
6	21	100.0	384	10	BE396917

7	21	100.0	477	9	AI682259
8	21	100.0	776	10	BE513300
9	21	100.0	910	12	BE881835
10	21	100.0	918	14	BQ437571
11	21	100.0	3100	11	BC019258
12	20	95.2	121	9	AA836048
13	18.4	87.6	178	9	AA683695
14	18.4	87.6	347	9	AA003676
15	18.4	87.6	356	14	W71682
16	18.4	87.6	446	10	AW318369
17	18.4	87.6	489	9	AA547497
18	18.4	87.6	573	10	BE639276
19	18.4	87.6	600	12	BE803155
20	18.4	87.6	600	13	BI986515
21	18.4	87.6	601	9	AA522010
22	18.4	87.6	632	10	BB611741
23	18.4	87.6	632	10	BB612512
24	18.4	87.6	648	10	BB657710
25	18.4	87.6	712	11	AK011797
26	18.4	87.6	749	14	BQ180708
27	18.4	87.6	895	14	BQ930512
28	18.4	87.6	930	14	BQ895257
29	18.4	87.6	2202	11	AK011689
30	17.8	84.8	195	17	AQ347018
31	17.8	84.8	325	13	BI477406
32	17.8	84.8	441	12	BF776116
33	17.4	82.9	195	9	AT000448
34	17.4	82.9	499	10	BB757949
35	17	81.0	332	17	AZ743062
36	17	81.0	334	13	BJ158403
37	17	81.0	418	10	AW497094
38	17	81.0	612	17	AZ667042
39	17	81.0	631	13	BJ165180
40	17	81.0	718	17	BH377427
41	17	81.0	763	17	BH527295
42	17	81.0	781	17	BH432699
43	16.8	80.0	108	12	BF377514
44	16.8	80.0	316	12	BG233936
45	16.8	80.0	322	12	BG373492

ALIGNMENTS

RESULT 1
BE560346
LOCUS BE560346 360 bp mRNA linear EST 15-AUG-2000
DEFINITION GO1346615F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687722 5', mRNA sequence.
ACCESSION BE560346
VERSION BE560346.1 GI:9804066
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 360)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM379 row: m column: 03
High quality sequence start: 4
High quality sequence stop: 360.
Location/Qualifiers
1. .360

BE560346 601346615F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687722 5',
mRNA sequence.
BE560346
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM379 row: m column: 03
High quality sequence start: 4
High quality sequence stop: 360.
Location/Qualifiers
1. .360

Sequence	Matches	Mismatches	Indels	Gaps
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2	0	0	0	0
3	0	0	0	0
4	0	0	0	0
5	0	0	0	0
6	0	0	0	0
7	0	0	0	0
8	0	0	0	0
9	0	0	0	0
10	0	0	0	0
11	0	0	0	0
12	0	0	0	0
13	0	0	0	0
14	0	0	0	0
15	0	0	0	0
16	0	0	0	0
17	0	0	0	0
18	0	0	0	0
19	0	0	0	0
20	0	0	0	0
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22	0	0	0	0
23	0	0	0	0
24	0	0	0	0
25	0	0	0	0
26	0	0	0	0
27	0	0	0	0
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89	0	0	0	0
90	0	0	0	0
91	0	0	0	0
92	0	0	0	0
93	0	0	0	0
94	0	0	0	0

1 GAAAGTATCTTCAAGGACGCC 21
|||
286 GAAAGTATCTTCAAGGACGCC 306

RESULT 3	361 bp	linear	EST 15-AUG-2000
BBE560268	BBE560268	mRNA	
LOCUS	60134608F1 NIH_MGC_8 Homo sapiens	cdna clone	IMAGE:3678885 5',
DEFINITION	mRNA sequence.		

ACCESSION
BES60268
VERSION
BES60268.1
KEYWORDS
EST.
human.
source

SCIENTIFIC ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 361)
 REFERENCE
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health
 AUTHORS
 National Institutes of Health
 TITLE
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.

1 (bases 1 to 361)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 COMMENT

Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LINC356 row: 1 column: 22
High quality sequence start: 4
High quality sequence stop: 361.

FEATURES	Location/Qualifiers
source	1. .361

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3678885"
/clone.lib="NIH MGC 8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
98 a 85.c 75 q 113 t

```

	BASE COUNT	ORIGIN	Score 21:	DB 10:	Length 361:
98 a	98 b	98 c	100 0%:		

Query Match	Score	Score
Best Local Similarity	100.0%;	Pred. No. 3.4;
Best Local Similarity	100.0%;	Mismatches 0;
Indels	0;	Gaps 0;

1 GAAAGTATCTTCAAGGCGCC 21
 QY |||||
 286 GAAAGTATCTTCAAGGCGCC 306
 QY |||||

Year	Male (millions)	Female (millions)
1990	105	100
2000	105	105
2010	100	105

RESULT 4
BE396918
165 bp
linear
mRNA
EST 21-JUL-2000

LOCUS
DEFINITION
601289477F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620058 5',
mRNA sequence.

ACCESSION BE396918
VERSION BE396918.1 GI:9342283

KEYWORDS EST.
SOURCE human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3687722"
/clone_lib="NIH MGC 8"

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/tissue_type="Burkitt lymphoma"
 /lab_host="PH108 (phage-resistant)"
 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)".

```

Query Match      100.0%; Score 21; DB 10; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 21; Conservative .0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GAAGTATCTCTCAAGGAGGCC 21
      |||||

```

```

Query matn. Similarity 100.0%; Pred. No. 3.4;
Best local similarity 100.0%; Mismatches 0; Gaps 0;
Matches 21; Conservative 0; Indels 0;
QY      1 CAAAGTATCTTCACGAGCGCC 21
          |||||

```

Db 285 GAAAGTATCTTCAAGGACGCC 306

RESULT 2
BE269531 361 bp mRNA : linear EST 13-JUL-2000
LOCUS 601184745P1 NIH_MGC 8 Homo sapiens CDNA clone IMAGE:3542483 5',
DEFINITION mRNA sequence.
ACCESSION BE269531 1 GI:9143153

VERSION
KEYWORDS
EST.
BE000001.1 01/01/2000

ORGANISM	REFERENCE	AUTHORS	TITLE	COMMENT
<i>Homo sapiens</i>				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1 (bases 1 to 361)				
NIH-MGC http://mgc.nci.nih.gov/ .				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: cgapbs-remail.nih.gov				
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.				
cDNA library Preparation: Ling Hong/Rubin Laboratory				
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
DNA Sequencing by: Incyte Genomics, Inc.				
Clone distribution: MGC clone distribution information can be				
seen through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov				

round through the 2.1mm entrance.
Plate: L1CM234 row: 1 column: 12
High quality sequence stop: 361.
High quality sequence stop: 361.

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FEATURES
Location/Qualifiers
1. 361
source
/organism="Homo sapiens"

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/ol>
/db_xref="taxon:9606"
/clone="IMAGE:3542483"
/clone_lib="NIH MGC 8"
/-issue type="Burkitt lymphoma"

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```

/abstract_1="Phage-resistant"
/lab host="DH10B (phage-resistant)"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
directionally"

```

ECORI; cDNA made by oligo-*a*T priming. Bidirectional clones into EcorI/XhoI sites using the following 5'-3'-sequences: GCGGACAG(C) size-selected >500bp for average

adaptor: GGAACGAG(9). Size of the insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT	88 a	85 c	75 g	113 f
ORIGIN				

Query Match	100.0%;	Score 21;	DB 10;	Length 361;
Best local similarity	100.0%;	Pred. No. 3.4;		

DEPT LOCAL SANITARIETY

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REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW291 row: 1 column: 19
High quality sequence start: 26
High quality sequence stop: 366.
FEATURES
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1..366
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/db_xref="taxon:9606"
/clone="IMAGE:3620058"
/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT 89 a 87 c 76 g 114 t
ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGAGCC 21
|||||
Db 291 GAAAGTATCTTCAAGGAGCC 311

RESULT 5
BE560799
LOCUS BE560799
DEFINITION 601346251F1 NIH_MGC_8 Homo sapiens CDNA clone IMAGE:3679476 5',
mRNA sequence.
ACCESSION BE560799
VERSION BE560799.1 GI:9804519
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE BE560799 371 bp mRNA linear EST 15-AUG-2000
601346251F1 NIH_MGC_8 Homo sapiens CDNA clone IMAGE:3679476 5',
mRNA sequence.
ACCESSION BE560799
VERSION BE560799.1 GI:9804519
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW358 row: e column: 13
High quality sequence start: 6
High quality sequence stop: 371.
FEATURES
source
1..371
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3620058"
/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3679476"
/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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```

BASE COUNT 90 a 94 c 75 g 112 t
ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGAGCC 21
|||||
Db 296 GAAAGTATCTTCAAGGAGCC 316

RESULT 6
BE396917
LOCUS BE396917
DEFINITION 601289473F1 NIH_MGC_8 Homo sapiens CDNA clone IMAGE:3619866 5',
mRNA sequence.
ACCESSION BE396917
VERSION BE396917.1 GI:9342282
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM291 row: a column: 19
High quality sequence start: 49
High quality sequence stop: 384.
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source
1..384
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3619866"
/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 90 a 93 c 80 g 121 t
ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 384;

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Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGAGCC 21
DB 309 GAAAGTATCTTCAAGGAGCC 329

RESULT 7
AI682259
LOCUS
DEFINITION
  wa71h05.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
  IMAGE:2301657 3', similar to TR:000425 O00425 PUTATIVE RNA BINDING
  PROTEIN KOC 1, mRNA sequence.
ACCESSION
  AI682259
KEYWORDS
  AI682259.1 GI:4892441
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 477)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
JOURNAL
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps@mail.nih.gov
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Insert Length: 608 Std Error: 0.00
  Seq primer: -40UP from Gibco
  High quality sequence stop: 427.
  Location/Qualifiers
    1..477
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:2301657"
      /clone_lib="Soares_NFL_T_GBC_S1"
      /lab_host="DH108"
      /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
      a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
      Equal amounts of plasmid DNA from three normalized
      libraries (fetal lung NBH19W, testis NHT, and B-cell
      NCI CGAP GCBI) were mixed, and ss circles were made in
      vitro. Following HAP purification, this DNA was used as
      tracer in a subtractive hybridization reaction. The driver
      was PCR-amplified cDNAs from pools of 5,000 clones made
      from the same 3 libraries. The pools consisted of
      I.M.A.G.E. clones 297480-302087, 682632-687239,
      726408-728711, and 729096-731399. Subtraction by Bento
      Soares and M. Fatima Ronaldo."
    BASE COUNT 122 a 99 c 102 g 153 t 1 others
  ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 477;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGAGCC 21
DB 355 GAAAGTATCTTCAAGGAGCC 375

RESULT 8
BE513300
LOCUS
DEFINITION
  601315375F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3633810 5',
  mRNA sequence.
ACCESSION
  BE513300
VERSION
  BE513300.1 GI:9720512
KEYWORDS
  EST.
SOURCE
  human.

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FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3908590"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT      252 a 222 c 241 g 194 t      1 others
ORIGIN
Query Match      100.0%; Score 21; DB 12; Length 910;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
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Db 311 GAAAGTATCTTCAAGGACGCC 331

RESULT 10
LOCUS      BQ437571      918 bp      mRNA      linear      EST 24-MAY-2002
DEFINITION AGENCOURT_7898330 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6154021
5', mRNA sequence.
ACCESSION  BQ437571
VERSION     BQ437571.1 GI:21176647
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM13494 row: 9 column: 14
High quality sequence stop: 555.
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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6154021"
/clone_lib="NIH_MGC_67"
/tissue_type="rctingblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
BASE COUNT      237 a 225 c 232 g 224 t
ORIGIN
Query Match      100.0%; Score 21; DB 14; Length 918;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
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Db 322 GAAAGTATCTTCAAGGACGCC 342

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RESULT 11
LOCUS      BC019258      3100 bp      mRNA      linear      HTC 19-DEC-2001
DEFINITION Homo sapiens, Similar to IGF-II mRNA-binding protein 3, clone
IMAGE:3542483, mRNA.
ACCESSION  BC019258
VERSION     BC019258.1 GI:17939534
KEYWORDS   HTC.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3100)
Strausberg.R.
Direct Submission.
Submitted (13-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA.
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Fawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAL Plate: 8 Row: c Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 5729900
This clone has the following problem: incomplete processing.
FEATURES
Source
Location/Qualifiers
1..3100
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3542483"
/tissue_type="Lymph, Burkitt lymphoma"
/clone_lib="NIH_MGC_8"
/lab_host="DH10B-R"
/notes="Vector: pOTB7"
BASE COUNT      748 a 674 c 873 g 805 t
ORIGIN
Query Match      100.0%; Score 21; DB 11; Length 3100;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGTATCTTCAAGGACGCC 21
|||||
Db 305 GAAAGTATCTTCAAGGACGCC 325

RESULT 12
LOCUS      AA836048      121 bp      mRNA      linear      EST 31-MAR-1998
DEFINITION O443C04.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1370694
similar to TR:O00425 O00425 PUTATIVE RNA BINDING PROTEIN KOC ;,
mRNA sequence.
ACCESSION  AA836048
VERSION     AA836048.1 GI:2910367

```


IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:262634

Seq primer: ETPPrimer

High quality sequence stop: 333.

FEATURES

source

Location/Qualifiers

1..347
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:437298"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stages="13.5-14.5dpc total fetus"
/lab_hosts="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "

81 a 92 c 100 g 74 t

BASE COUNT
ORIGIN

Query Match 87.6%; Score 18.4; DB 9; Length 347;

Best Local Similarity 95.0%; Pred. No. 75;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGACGC 20

Db 168 GAAAGTGTCTTCAAGGACGC 187

RESULT 15

W71682

LOCUS

DEFINITION ms34c05.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA

clone IMAGE:389384 5', mRNA sequence.

W71682

VERSION

W71682.1 GI:1380423

KEYWORDS

SOURCE

house mouse.

Mus musculus

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:241216

Seq primer: ETPPrimer

High quality sequence stop: 354.

Location/Qualifiers

1..356

source

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:389384"

/clone_lib="Soares mouse embryo NbME13.5 14.5"

/sex="unknown"

/tissue_type="embryo"

/dev_stages="13.5-14.5dpc total fetus"

/lab_hosts="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "

79 a 93 c 93 g 91 t

BASE COUNT
ORIGIN

Query Match 87.6%; Score 18.4; DB 14; Length 356;

Best Local Similarity 95.0%; Pred. No. 76;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGTATCTTCAAGGACGC 20

Db 322 GAAAGTGTCTTCAAGGACGC 341

Search completed: April 18, 2003, 07:31:44

Job time : 737.348 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:46:26 ; Search time 292 Seconds
(without alignments)
2192.677 Million cell updates/sec

Title: US-09-270-437D-10

Perfect score: 22
Sequence: 1 ctgcaagggttttctgtggcg 22

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.ov.*
- 5: gb.pat.*
- 6: gb.ph.*
- 7: gb.pl.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.un.*
- 12: gb.vi.*
- 13: gb.vi.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
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- 22: em.ov.*
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- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
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- 35: em.htg_rod.*
- 36: em.htg_ram.*
- 37: em.htg_vrt.*
- 38: em.ey.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	100.0	1740	6	AX365954 Sequence
C 2	22	100.0	1743	6	AX366054 Sequence
C 3	22	100.0	1743	6	AX366057 Sequence
C 4	22	100.0	1764	6	AX366035 Sequence
C 5	22	100.0	4155	9	HSU76705
C 6	22	100.0	4159	9	ARI17863
C 7	22	100.0	4171	9	AF117108
C 8	22	100.0	4181	6	AX333233
C 9	22	100.0	4181	6	AX365782
C 10	22	100.0	4181	9	HSU97188
C 11	22	100.0	4602	6	AX397963
C 12	22	100.0	104668	9	AC021876
C 13	22	100.0	158105	2	AC023375
C 14	18.8	85.5	98951	2	AC090069
C 15	18.8	85.5	200956	9	AC104165
C 16	18.8	85.5	208197	9	AC009107
C 17	18.4	83.6	111764	9	AL133379
C 18	18.4	83.6	156422	2	AC106309
C 19	18.4	83.6	159082	9	AC025947
C 20	18.4	83.6	163404	2	AL355308
C 21	18.4	83.6	172777	9	AC026395
C 22	18	81.8	79554	8	NCB11B23
C 23	17.8	80.9	32145	2	AC113360
C 24	17.8	80.9	58511	2	AC097402
C 25	17.8	80.9	91200	9	AF001152
C 26	17.8	80.9	140666	9	AC120114
C 27	17.8	80.9	141085	2	AC097250
C 28	17.8	80.9	147556	2	AC011007
C 29	17.8	80.9	157481	9	AC093512
C 30	17.8	80.9	173235	2	AC023756
C 31	17.8	80.9	183666	9	AC009487
C 32	17.8	80.9	189947	2	AC062035
C 33	17.8	80.9	191076	2	AC115786
C 34	17.8	80.9	203770	9	AC082651
C 35	17.8	80.9	235669	2	AC096932
C 36	17.4	79.1	56509	9	AL353700
C 37	17.4	79.1	83596	2	AC095682
C 38	17.4	79.1	94180	2	AC106942
C 39	17.4	79.1	150722	2	AC120491
C 40	17.4	79.1	154218	9	AC020663
C 41	17.4	79.1	165777	2	AC111441
C 42	17.4	79.1	168085	9	AC027687
C 43	17.4	79.1	181347	2	AC117303
C 44	17.4	79.1	214042	2	AC093028
C 45	17.4	79.1	258120	2	AC114408

ALIGNMENTS

RESULT 1
AX365954/c
LOCUS AX365954
DEFINITION Sequence 347 from Patent WO0200174.
ACCESSION AX365954
VERSION AX365954.1 GI:18697455
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wang, T., Wang, A., Skeiky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A., McNeill, P.D., Fanger, N., Retter, M.W., Marnierakis, M., Fanger, G.R., Vedwick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.

AX365954 Sequence 347 from Patent WO0200174.
1740 bp DNA linear PAT 16-FEB-2002

Mon Apr 21 10:29:39 2003

Compositions and methods for the therapy and diagnosis of lung

TITLE
Cancer
JOURNAL
Patent: WO 0200174-A 347 03-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
1. .1740
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 526 a 406 c 417 g 391 t
ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 1740;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGTCTGGCG 22
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Db 498 CTGCAAGGGGTTTGTCTGGCG 477
RESULT 2
AX366054/c 1743 bp DNA linear PAT 15-FEB-2002
LOCUS
Sequence 447 from Patent WO0200174.
DEFINITION
ACCESSION AX366054
VERSION AX366054.1 GI:18697498
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Wang, T., Wang, A., Skeiky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A., McNeill, P.D., Fanger, N., Retter, M.W., Marnerakis, M., Fanger, G.R., Vedvick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.
AUTHORS
TITLE Compositions and methods for the therapy and diagnosis of lung
JOURNAL
Patent: WO 0200174-A 447 03-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
1. .1743
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 527 a 406 c 418 g 392 t
ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 1743;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
Db 498 CTGCAAGGGGTTTGTCTGGCG 477
RESULT 3
AX366057/c 1743 bp DNA linear PAT 15-FEB-2002
LOCUS
Sequence 450 from Patent WO0200174.
DEFINITION
ACCESSION AX366057
VERSION AX366057.1 GI:18697500
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Wang, T., Wang, A., Skeiky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A., McNeill, P.D., Fanger, N., Retter, M.W., Marnerakis, M., Fanger, G.R., Vedvick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.
AUTHORS
TITLE Compositions and methods for the therapy and diagnosis of lung
JOURNAL
Patent: WO 0200174-A 450 03-JAN-2002;

FEATURES
source
Location/Qualifiers
1. .1743
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 527 a 406 c 418 g 392 t
ORIGIN
Query Match 100.0%; Score 22; DB 6; Length 1743;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
Db 498 CTGCAAGGGGTTTGTCTGGCG 477
RESULT 4
AX366035/c 1764 bp DNA linear PAT 15-FEB-2002
LOCUS
Sequence 428 from Patent WO0200174.
DEFINITION
ACCESSION AX366035
VERSION AX366035.1 GI:18697484
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Wang, T., Wang, A., Skeiky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A., McNeill, P.D., Fanger, N., Retter, M.W., Marnerakis, M., Fanger, G.R., Vedvick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.
AUTHORS
TITLE Compositions and methods for the therapy and diagnosis of lung
JOURNAL
Patent: WO 0200174-A 428 03-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
1. .1764
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGTCTGGCG 22
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Db 519 CTGCAAGGGGTTTGTCTGGCG 498
RESULT 5
HSU76705/c 4155 bp mRNA linear PRI 26-JAN-1999
LOCUS
Human putative RNA binding protein Koc1 mRNA, complete cds.
DEFINITION
ACCESSION U76705
VERSION U76705.1 GI:4098296
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4155)
Mueller-Pillasch, F., Lacher, U. and Wallrapp, C.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1996) Innere Medizin I, University of Ulm, Robert-Koch-Str.8, Ulm 89081, Germany
FEATURES
source
Location/Qualifiers
1. .4155
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"

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/map="7p11.5"
/cell_line="Patau988s"
/tissue_type="pancreas"
251..1390
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/notes="Kh-domain containing protein; overexpressed in
cancer"
/codon_start=1
/product="Koc1"
/protein_id="A098297"
/db_xref="GI:4098297"
/translation="MNKLYGNLSNAAPSDLESIFDKAKIPVSGPFLVKTGYAFVDC
PDSWALKATKALSGKIEHKGPIEVEHSPKQRIKQIRNIPPHLQWEVLDSLLV
QYGVSECEQNTDSETAVVNTYSSKQARQALDKLNGFLENFLKVAIYIDENAA
QQPQQPQRGRLGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG
RNTTKQSKIDVHRKENAGAEKSTILSTPGTSAACKSILEIMHKEAQDIKFTTE
IPLKILAHNNFVGRLLGKGRNLKIEQDITDKITISPLQELTLNPERITVKGVE
TCABEEIMKKIRESYENDIASMNLAHLIPLGNLNLGLPFTSGMPPTSGPPSA
MTPPYQPEQSETVHQPALSGAIIKQGHKQSRFAGASIKIAPAEAPDAK
VRNVIITGPPEAQKAGRIYKIKKEENFVSPKEVKEAHIRVPSFAAGRVIGKGG
TVNELQNLSSAEVVRDQTPDENDQVVVKITGHFYACQVQAKRIQELTVQKQHQQ
KALQSGPPOSRRK"
BASE COUNT 1277 a 830 c 851 g 1181 t 16 others
ORIGIN

Query Match 100.0%; Score 22; DB 9; Length 4155;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
Db 748 CTGCAAGGGGTTTGTCTGGGCG 727

RESULT 6
AR171863/c
LOCUS AR171863 4159 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 4 from patent US 6297364.
ACCESSION AR171863
VERSION AR171863.1 GI:17910813
KEYWORDS
SOURCE Unknown.
REFERENCE 1 (bases 1 to 4159)
AUTHORS Chen, Y.-T., Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K.
and Old, L.J.
TITLE Isolated nucleic acid molecule encoding cancer associated antigen,
the antigen itself, and uses thereof
JOURNAL Patent: US 6297364-A 4 02-OCT-2001;
FEATURES Location/Qualifiers
SOURCE 1..4159
/organism="unknown"
BASE COUNT 1281 a 830 c 851 g 1181 t 16 others
ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 4159;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
Db 748 CTGCAAGGGGTTTGTCTGGGCG 727

RESULT 7
AF117108/c
LOCUS AF117108 4171 bp mRNA linear PRI 26-JAN-1999
DEFINITION Homo sapiens IGF-II mRNA-binding protein 3 (IMP-3) mRNA, complete
cde.
ACCESSION AF117108
VERSION AF117108.1 GI:4191611
KEYWORDS
```

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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4171)
AUTHORS Nielsen, J., Christensen, J., Lykke-Andersen, J., Johnsen, A.H.,
Wewer, U.M., and Nielsen, F.C.
TITLE A family of insulin-like growth factor II mRNA-binding proteins
represses translation in late development
JOURNAL Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
MEDLINE 99108099
PUBMED 9891060
REFERENCE 2 (bases 1 to 4171)
AUTHORS Nielsen, J., Christensen, J., Lykke-Andersen, J., Johnsen, A.H.,
Wewer, U.M., and Nielsen, F.C.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
FEATURES Location/Qualifiers
SOURCE 1..4171
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..4171
/gene="IMP-3"
267..2006
/gene="IMP-3"
/notes="binds multiple sites in IGF-II mRNA 5'UTR;
identical to KH-domain containing protein overexpressed in
cancer (koc)"
/codon_start=1
/product="IGF-II mRNA-binding protein 3"
/protein_id="A09828.1"
/db_xref="GI:4191612"
/translation="MNKLYGNLSNAAPSDLESIFDKAKIPVSGPFLVKTGYAFVDC
PDSWALKATKALSGKIEHKGPIEVEHSPKQRIKQIRNIPPHLQWEVLDSLLV
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QQPQQPQRGRLGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG
RNTTKQSKIDVHRKENAGAEKSTILSTPGTSAACKSILEIMHKEAQDIKFTTE
IPLKILAHNNFVGRLLGKGRNLKIEQDITDKITISPLQELTLNPERITVKGVE
TCABEEIMKKIRESYENDIASMNLAHLIPLGNLNLGLPFTSGMPPTSGPPSA
MTPPYQPEQSETVHQPALSGAIIKQGHKQSRFAGASIKIAPAEAPDAK
VRNVIITGPPEAQKAGRIYKIKKEENFVSPKEVKEAHIRVPSFAAGRVIGKGG
TVNELQNLSSAEVVRDQTPDENDQVVVKITGHFYACQVQAKRIQELTVQKQHQQ
KALQSGPPOSRRK"
BASE COUNT 1292 a 822 c 853 g 1199 t 5 others
ORIGIN

Query Match 100.0%; Score 22; DB 9; Length 4171;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
Db 764 CTGCAAGGGGTTTGTCTGGGCG 743

RESULT 8
AX333233/c
LOCUS AX333233 4181 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 3742 from Patent WO0194629.
ACCESSION AX333233
VERSION AX333233.1 GI:18123867
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R., and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3742 13-DEC-2001;
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[illegible]

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/db_xref="GI:21260819"
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PDSWALKALREALSGKIELHGKPIEVHSGVPRQIRKQIRNIPHLQWEVLDSLLV
QYGVSCQVQDTSATVAVNVVYSSKQARQALDKLNGFLENFTLKVAYIPDEMAA
QNPLOQPRRGLGSGRSGQSPGSKQKCDPLRLVLPVTOVGAIIGKEGATI
RNTTKQTQSDIVHRENAGAASIKITILSTPGTSAACKSILEIMHKEAQDIKTEE
IPUKIAHNHNVGRLLKKEGRNKKIEQDQTDKITISPLQELTLNPERTIYVGNVE
TCABAEIEMKKIRSEYENDIASMNLOHMLIFGLNUNALGLPFTSGMPPPTSGPPSA
MTYPYQFQSESETVHQFIPALSVGAILIGKQGHKQLSRFAGASIKIAPAEAPDAK
VRVIELQSPPEAFKAGRIYKIKENFVSPKEEYKLEAHIRVSPFAGRVIKGGGK
TVNELNLSAEAVVPRDQTPDENDQVVVKITGHFYACQVQAKIQEILTVQKQHQQ
KALQSGPPQSRRR"
BASE COUNT 1463 a 907 c 918 g 1298 t 16 others
ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 4602;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
Db 1169 CTGCAAGGGGTTTGTCTGGGCG 1148

RESULT 12
AC021876 104668 bp DNA linear PRI 04-JUN-2002
LOCUS Homo sapiens BAC clone GS1-117B4 from 7, complete sequence.
DEFINITION
AC021876
ACCESSION
VERSION AC021876.5 GI:13446341
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 104668)
Suleston,J.E. and Waterston,R.H.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
PUBMED 9847074
2 (bases 1 to 104668)
Du,F., Stonaking,T. and Moeller,D.
The sequence of Homo sapiens BAC clone GS1-117B4
Unpublished (2001)
3 (bases 1 to 104668)
Waterston,R.H.
Direct Submission
Submitted (21-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 104668)
Waterston,R.H.
Direct Submission
Submitted (03-AUG-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 104668)
Waterston,R.H.
Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 104668)
Waterston,R.H.
Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (bases 1 to 104668)
Waterston,R.H.
Direct Submission

```

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Submitted (25-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
8 (bases 1 to 104668)
Waterston,R.
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
9 (bases 1 to 104668)
Waterston,R.
Direct Submission
Submitted (04-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 25, 2001 this sequence version replaced gi:9665195.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics

Center project name: H_GS117B04

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and
sequencing collaboration between the NHGRI Chromosome 7 Mapping
Project (Eric D. Green, Director), John D. McPherson in the
Department of Genetics (Washington University), and the Washington
University Genome Sequencing Center. For additional information
about the map position of this sequence, see
http://www.nhgri.nih.gov/DIR/GRB/CHR7 send
mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

This clone is from the first BAC library from Genome Systems, Inc.
(http://www.genomesystems.com).

Cell line: lymphoblastoid

Haplotypes: two

VECTOR: pBeloBAC

Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is CTA-271G13, 200 bp overlap; the
clone sequenced to the right is AC023375. Actual start of this
clone is at base position 102112 of CTA-271G13; actual end is at
base position 104668 of GS1-117B4.

The sequence from 80185 to 80225 was derived from PCR product of
GS1-117B4 BAC DNA.

FEATURES
source

1. .104668
Location/Qualifiers
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/db_xrefs="taxon:9606"
/chromosomes="7"
/map="7"
/clone="GS1-117B4"
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1042..1339
repeat_region
misc_feature
1733..2070

misc_feature	12928..13050	/note="similar to EST BF241103 (NID:g11155028)"
misc_feature	12945..13050	/note="similar to EST AV612377 (NID:g9748047)"
repeat_region	13115..13172	/rpt family="L2"
repeat_region	13571..13877	/rpt family="Alu"
misc_feature	14561..14722	
Query Match	100.0%;	Score 22; DB 9; Length 104668;
Best Local Similarity	100.0%;	Pred. No. 4.1;
Matches	22; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	CTGCAAGGGGTTTGTCTGGGCG 22
Db	18478	CTGCAAGGGGTTTGTCTGGGCG 18499
RESULT 13		
AC023375		158105 bp DNA linear HTG 24-AUG-2002
LOCUS	AC023375	
DEFINITION	Homo sapiens chromosome 7, clone RP11-571M6 map 7, WORKING DRAFT	
ACCESSION	AC023375.2	GI:7209933
VERSION	AC023375	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 158105)	
TITLE	Birren, B., Linton, L., Nusbaum, C. and Lander, E.	
JOURNAL	Homo sapiens chromosome 7, clone RP11-571M6	
REFERENCE	Unpublished	
AUTHORS	2 (bases 1 to 158105)	
	Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bada, F., Boguslavsky, L., Bouchgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Fenesstor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczy, J., Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mieng, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivat, T.M., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tefaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zaincoun, J., Zimmer, A. and Zody, M.	
TITLE	Direct Submission	
JOURNAL	Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
REFERENCE	3 (bases 1 to 158105)	
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F., Boguslavsky, L., Bouchgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., FitzHugh, W., Gage, D., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,	


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/misc_feature
/note="assembly_fragment"
16535..18900

Query Match
Best Local Similarity 100.0%; Score 22; DB 2; Length 158105;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTCTGGGCG 22
|||||
Db 148579 CTGCAAGGGGTTTCTGGGCG 148600

RESULT 14
AC090069 98951 bp DNA linear HTG 20-APR-2001
LOCUS Homo sapiens chromosome 5 clone CTD-2162G15, WORKING DRAFT
DEFINITION SEQUENCE, 7 unordered pieces.
AC090069
AC090069.1 GI:12830173
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
VERSION
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 98951)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 98951)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 689916
Center clone name: CITB-H1_2162G15
-----
Summary Statistics
Consensus quality: 91863 bases at least Q40
Consensus quality: 96729 bases at least Q30
Consensus quality: 97483 bases at least Q20
Estimated insert size: 103000; agarose-fp estimation
Estimated insert size: 98351; sum-of-contigs estimation
Quality coverage: 5.97 in Q20 bases; agarose-fp estimation
Quality coverage: 5.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1640: contig of 1640 bp in length
* 1641 1740: gap of unknown length
* 1741 4817: contig of 3077 bp in length
* 4818 4917: gap of unknown length
* 4918 10479: contig of 5562 bp in length
* 10480 10579: gap of unknown length
* 10580 17185: contig of 6606 bp in length
* 17186 17285: gap of unknown length
* 17286 27136: contig of 9851 bp in length
* 27137 27236: gap of unknown length
* 27237 53446: contig of 26110 bp in length
* 53447 53447: gap of unknown length
* 53447 98951: contig of 45505 bp in length.

FEATURES
Location/Qualifiers
1..98951

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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2162G15"
/clone_lib="Caltech human BAC library D"
28584 a 22060 c 20767 g 26935 t 605 Others
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 85.5%; Score 18.8; DB 2; Length 98951;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTCTGGGCG 22
|||||
Db 10782 CTGCAAGGGGTTTCTGTGAG 10803

RESULT 15
AC104165 200956 bp DNA linear PRI 27-JUN-2002
LOCUS Homo sapiens chromosome 3 clone RP11-68104, complete sequence.
DEFINITION AC104165 AC068625
AC068625
AC104165.2 GI:21617715
VERSION
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 200956)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 200956)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE
3 (bases 1 to 200956)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 27, 2002 this sequence version replaced gi:17352429.
-----Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgctgs@u.washington.edu
Drafting Center: WUGSC
-----Project Information
Center project name: chr-3
Center clone name: RP11-68104 (bc0528)
-----Summary Statistics
Sequencing vector: unknown; 42% of reads
Sequencing vector: plasmid; 58% of reads
Chemistry: Dye-terminator ET; 80% of reads
Chemistry: Dye-terminator Big Dye; 20% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 200732 bases at least Q40
Consensus quality: 200909 bases at least Q30
Consensus quality: 200947 bases at least Q20
Insert size: 200956; sum-of-contigs
Quality coverage: 10.4x in Q20 bases; sum-of-contigs
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Overlapping Sequences:
5': RP11-348P10 (UWGC:bc0377) AC124045
3': RP11-578F5 (UWGC:bc0477) AC105902, 95352-bp overlap
-----
Sequence Quality Assessment:

```


This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BgIII			EcoRI			HindIII		
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap
5328	5288	8696	8571	3534	3560			
2067	2057	6	<800	6382	6318			
6846	6934	6068	6154	512	<800			
144	<800	11400	11207	449	<800			
1459	1439	96	<800	5736	5646			
70	<800	4100	4106	2978	3031			
3690	3725	779	760	8146	8133			
102	<800	1221	1170	4465	4477			
511	<800	278	<800	2239	2257			
1903	1919	8458	8571	45	<800			
5124	5028	12014	11879	4368	4477			
367	<800	645	<800	286	<800			
7100	6934	1177	1170	4633	4784			
5890	5889	153	<800	1462	1405			
1814	1816	1993	1932	2058	2110			
125	<800	3153	3186	745	<800			
43	<800	132	<800	1321	1243			
117	<800	4939	4965	3528	3560			
1955	1919	466	<800	1640	1662			
3477	3529	1311	1279	8779	8765			

4899	5028	3183	3186	5089	4991
774	799	16952	16678	2571	2631
10749	10616	1629	1629	2440	2446
1620	1602	7261	7427	1682	1662
8868	8810	7837	7939	1660	1662
5884	5889	3940	4106	4912	4991
1521	1529	756	760	2470	2446
771	799	2395	2496	8892	8765
11706	11675	5310	5399	1257	1243
369	<800	21139	21498	10114	9869
5177	5288	4082	4106	14019	14339
2916	2950	7866	7939	3580	3560
137	<800	7411	7427	3022	3031
2406	2347	3378	3366	8296	8133
3857	3725	7272	7427	3319	3311
5249	5288	3059	3186	1694	1662
5343	5288	8214	8571	1747	1662
6819	6934	5836	5849	2370	2446
2335	2347	5394	5399	4817	4784
569	<800	419	<800	1139	1073
135	<800	3260	3186	3946	3909
3825	3725	2082	2097	12931	12902
6741	6934	8568	8571	2109	2110
1472	1439	1681	1629	364	<800
3707	3725	741	760	78	<800
703	<800	2905	3005	254	<800
207	<800			6129	6318
5047	5028			1674	1662
1134	1133			1250	1243
1070	1069			4768	4784
4665	4675			1083	1073
1121	1133			1023	1073
6920	6934			2602	2631
3317	3264			2449	2446
1683	1697			1249	1243
3525	3529			7228	7182

Mon Apr 21 10:29:39 2003

Query Match 85.5%; Score 18.8; DB 9; Length 200956;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGTGGGCG 22
DB 27941 CTGCCAGGGGTTTGTGGGTG 27962

Search completed: April 18, 2003, 06:17:22
Job time : 385 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:12:35 ; Search time 98 Seconds
(without alignments)
505.551 Million cell updates/sec

Title: US-09-270-437D-10

Perfect score: 22

Sequence: 1 ctgcaagggttttctgtggcg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	22	100.0	22	21	PCR primer for DNA
C 2	22	100.0	282	22	Human bone marrow
C 3	22	100.0	282	22	Probe #25064 used
C 4	22	100.0	588	22	Human bone marrow
C 5	22	100.0	588	22	Probe #12084 used
C 6	22	100.0	1740	21	Human lung cancer-
C 7	22	100.0	1740	21	Human lung tumour
C 8	22	100.0	1743	24	Human lung tumour
C 9	22	100.0	1743	24	Human lung tumour

C 10	22	100.0	1764	24	ABL49283	Human lung tumour
C 11	22	100.0	4159	21	AAZ36150	DNA encoding cancer
C 12	22	100.0	4181	21	AAC65900	Human lung cancer-
C 13	22	100.0	4181	24	ABL65405	Lung cancer relate
C 14	22	100.0	4181	24	ABL49119	Human lung tumour
C 15	22	100.0	4601	24	ABA99958	Human KOC DNA. Ho
C 16	17.4	73.1	861	22	AAI39552	Human neuroblastom
C 17	17.2	78.2	255	22	AAH82149	Human KOC DNA. Ho
C 18	17.2	78.2	1206	21	AAH82149	DNA encoding novel
C 19	17.2	78.2	1206	21	AAH82149	DNA encoding novel
C 20	17.2	78.2	4264	23	AAS86150	DNA encoding novel
C 21	17.2	78.2	4264	23	ABL16312	Drosophila melanog
C 22	17.2	78.2	24494	21	AAZ31253	Bacterium 2412.1 f
C 23	17.2	78.2	302250	24	ABL67703	Oesophagus cancer
C 24	16.4	74.5	568	24	ABN64702	Human cancer relat
C 25	16.4	74.5	75899	24	ABK85261	Human genomic DNA
C 26	16.2	73.6	296	24	ABL72849	Corn tassal-derive
C 27	16.2	73.6	300	21	AAA00921	Human colon cancer
C 28	16.2	73.6	462	23	ABV55571	Human prostate exp
C 29	16.2	73.6	514	23	ABV54482	Human prostate exp
C 30	16.2	73.6	533	22	AAK77132	Human immune/haema
C 31	16.2	73.6	561	23	AAS70767	DNA encoding novel
C 32	16.2	73.6	782	20	AAZ17200	Human gene express
C 33	16.2	73.6	784	21	AAA02465	Human colon cancer
C 34	16.2	73.6	859	21	AAZ34953	Human acid triacylg
C 35	16.2	73.6	1563	24	ABN67088	Streptococcus poly
C 36	16.2	73.6	2286	23	ABU02757	Drosophila melanog
C 37	16.2	73.6	4739	23	ABU22680	Drosophila melanog
C 38	16.2	73.6	4750	23	ABU02756	Drosophila melanog
C 39	16.2	73.6	5547	20	AAW77524	E. coli strain DSM
C 40	16.2	73.6	5552	19	AAV61942	Plasmid pMD12 DNA.
C 41	16.2	73.6	6232	24	AAU42134	Human Kruppel-like
C 42	16.2	73.6	6232	24	AAU42134	Human Kruppel-like
C 43	16.2	73.6	9722	22	ABA15166	Human nervous syst
C 44	16.2	73.6	14855	22	ABA15164	Human nervous syst
C 45	16.2	73.6	22028	24	ABA93286	Human acetyl-Coenz

ALIGNMENTS

RESULT 1
AAZ36156
ID AAZ36156 standard; DNA; 22 BP.
XX
AC AAZ36156;
XX
DT 11-FEB-2000 (first entry)
XX
XX PCR primer for DNA encoding cancer associated antigen KOC-1.
DE
DE Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss.
XX
XX Synthetic.
OS
OS Homo sapiens.
XX
PN WO9954738-A1.
XX
PD 28-OCT-1999.
XX
PF 16-MAR-1999; 99WO-US05766.
XX
PR 17-APR-1998; 98US-0061709.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA
PI Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;
XX
XX WPI; 2000-013284/01.
XX
XX Nucleotides representing cancer-associated genes, used to develop
PT products for the diagnosis, monitoring and treatment of cancers -

PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 PT in a patient -

XX
 PS Claim 1a; Page 259-259; 261pp; English.

XX This invention describes a novel isolated polypeptide (1) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2, and then administered to the patient to inhibit
 CC development of cancer.

XX Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 other;

SQ Query Match 100.0%; Score 22; DB 21; Length 1740;

Best Local Similarity 100.0%; Pred. No. 0.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
 |||||
 Db 498 CTGCAAGGGGTTTGTCTGGCG 477

RESULT 7

ABL49254/c
 ID ABL49254 standard; cDNA; 1740 BP.

XX ABL49254;

XX 01-MAY-2002 (first entry)

XX Human lung tumour L523S cDNA sequence SEQ ID NO:347.

XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 XX immune response; ss.

XX Homo sapiens.

XX WO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

XX 02-AUG-2000; 2000US-0630940.

XX 21-AUG-2000; 2000US-0643597.

XX 15-SEP-2000; 2000US-0662786.

XX 09-OCT-2000; 2000US-0685696.

XX 12-DEC-2000; 2000US-0735705.

XX 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

XX McNeill PD, Fanger N, Ratter MW, Marnerakis M, Fanger GR;

XX Vedwick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI; 2002-090513/12.

XX P-PSDB; ABB74997.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating
 XX lung cancer or stimulating an immune response -

XX Example 2; Page 330; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.

XX Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 other;

SQ Query Match 100.0%; Score 22; DB 24; Length 1740;

Best Local Similarity 100.0%; Pred. No. 0.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
 |||||
 Db 498 CTGCAAGGGGTTTGTCTGGCG 477

RESULT 8

ABL49297/c
 ID ABL49297 standard; cDNA; 1743 BP.

XX ABL49297;

XX 01-MAY-2002 (first entry)

XX Human lung tumour L523S recombinant polynucleotide SEQ ID NO:447.

XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 XX immune response; ss.

XX Homo sapiens.

XX WO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

XX 02-AUG-2000; 2000US-0630940.

XX 21-AUG-2000; 2000US-0643597.

XX 15-SEP-2000; 2000US-0662786.

XX 09-OCT-2000; 2000US-0685696.

XX 12-DEC-2000; 2000US-0735705.

XX 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

XX McNeill PD, Fanger N, Ratter MW, Marnerakis M, Fanger GR;

XX Vedwick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI; 2002-090513/12.

XX P-PSDB; ABB75053.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating
 XX lung cancer or stimulating an immune response -

XX Claim 1; Page 367; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.

XX

XX DE DNA encoding cancer associated antigen KOC-1.
XX KW Cancer associated antigen; KOC-1; cancer; vaccine; CT7; ss.
XX OS Homo sapiens.
XX PN WO9954738-A1.
XX PD 28-OCT-1999.
XX PF 16-MAR-1999; 99WO-US05766.
XX PR 17-APR-1998; 98US-0061709.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Chen Y, Gure A, Teang S, Stockert E, Jager E, Knuth A, Old LJ;
XX DR WPI; 2000-013284/01.
XX PR Nucleotides representing cancer-associated genes, used to develop
XX PT products for the diagnosis, monitoring and treatment of cancers
XX PS Claim 88; Page 39-40; 44pp; English.
XX CC The present sequence represents a cancer associated antigen gene
XX CC designated KOC-1. The specification also describes a cancer associated
XX CC antigen designated CT7. The CT7 polynucleotide was isolated from
XX CC SK-MEL-37 melanoma cells. The polypeptide has some homology with
XX CC MAGE-10, limited to about 210 carboxy terminal amino acids. The amino
XX CC terminal of the protein has a repetitive pattern, with repeats rich in
XX CC serine, proline, glutamine and leucine, and an almost invariable core of
XX CC the peptide given in AAY43877. The CT7 polypeptide can be processed to
XX CC peptides which provoke lysis by cytolytic T cells. The polynucleotides
XX CC and polypeptides can be used for treating a cancerous condition and
XX CC screening for or diagnosing cancerous conditions. The cancer associated
XX CC antigens can be used as an immunogenic or vaccine composition with an
XX CC adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony
XX CC stimulating factor (GM-CSF).
XX SQ Sequence 4159 BP; 1281 A; 830 C; 851 G; 1181 T; 16 other;
Query Match 100.0%; Score 22; DB 21; Length 4159;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
DB 748 CTGCAAGGGGTTTGTCTGGGCG 727
RESULT 12
AAC65900/c
ID AAC65900 standard; cDNA; 4181 BP.
XX AC AAC65900;
XX XX
XX DT 21-FEB-2001 (first entry)
XX DE Human lung cancer-associated cDNA L523S.
XX KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX KW vaccine; detection; ss.
XX OS Homo sapiens.
XX PN WO200061612-A2.
XX PD 19-OCT-2000.
XX PF 03-APR-2000; 2000WO-US08896.
XX XX

PR 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX (CORI-) CORIXA CORP.
XX PI Wang T, Fan L;
XX DR WPI; 2000-628399/60.
XX DR P-PSDB; AAB11328.
XX PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
XX PT protein is used for detecting and monitoring progression of lung cancer
XX PT in a patient -
XX PS Claim 1a; Page 184-186; 261pp; English.
XX CC This invention describes a novel isolated polypeptide (I) which
XX CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
XX CC which have cytostatic activity. The polypeptides and polynucleotides are
XX CC used in compositions and vaccines to inhibit the development of cancer,
XX CC especially lung cancer, in a patient. Methods described in the invention
XX CC can be used to monitor the progression of a cancer by carrying out the
XX CC detection at subsequent time points and comparing the results from the
XX CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
XX CC are treated with P2, polynucleotides encoding P2 or antigen presenting
XX CC cells expressing P2, and then administered to the patient to inhibit
XX CC development of cancer.
XX SQ Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
Query Match 100.0%; Score 22; DB 21; Length 4181;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
DB 748 CTGCAAGGGGTTTGTCTGGGCG 727
RESULT 13
ABL65405/c
ID ABL65405 standard; DNA; 4181 BP.
XX AC ABL65405;
XX XX
XX DT 15-MAY-2002 (first entry)
XX DE Lung cancer related gene sequence SEQ ID NO:3742.
XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO200194629-A2.
XX PD 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US10838.
XX PR 05-JUN-2000; 2000US-209473P.
XX PR 05-JUN-2000; 2000US-209531P.
XX PR 18-SEP-2000; 2000US-233133P.
XX PR 18-SEP-2000; 2000US-233617P.
XX PR 20-SEP-2000; 2000US-234009P.
XX PR 20-SEP-2000; 2000US-234034P.
XX PR 20-SEP-2000; 2000US-234052P.
XX PR 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 27-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX PA (AVAL-) AVALON PHARM.
XX PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX PI Soppet DR, Weaver Z;
XX PI WPI; 2002-188264/24.
XX DR
XX XX
XX PT Screening for anti-neoplastic agent involves exposing cells to a
XX PT chemical agent to be tested for anti-neoplastic activity, and
XX PT determining a change in expression of a gene of a signature gene set
XX XX
XX PS Claim 1; SEQ ID 3742; 44pp; English.
XX XX
XX CC The present invention describes a method (M1) for screening for an
XX CC anti-neoplastic agent. The method involves exposing cells to a chemical
XX CC agent to be tested for anti-neoplastic activity, determining a change in
XX CC expression of at least one gene (1) of a signature gene set, where (1)
XX CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
XX CC to ABL70110), or is at least 95% identical to (S), where a change in
XX CC expression is indicative of anti-neoplastic activity. (1) has cytostatic
XX CC activity and can be used in gene therapy. M1 can be used for screening
XX CC an anti-neoplastic agent, and can be used for producing a product which
XX CC is the data collected with respect to the anti-neoplastic agent as a
XX CC result of M1, and the data is sufficient to convey the chemical
XX CC structure and/or properties of the agent. M1 can be used in the
XX CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
XX CC oesophageal, ovarian, kidney, prostate or pancreatic cancer.
XX CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
XX CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
XX CC carcinoma, papillary carcinoma and Wilms' tumour.
XX XX
XX SQ Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
Query Match 100.0%; Score 22; DB 24; Length 4181;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGTCTGGCG 22

Db 748 CTGCAAGGGGTTTGTCTGGCG 727
RESULT 14
ABL49119/c
ID ABL49119 standard; cDNA; 4181 BP.
XX AC ABL49119;
XX DT 01-MAY-2002 (first entry)
XX DE Human lung tumour LS23S cDNA sequence SEQ ID NO:175.
XX KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
XX OS immune response; ss.
XX OS Homo sapiens.
XX PN WO200200174-A2.
XX PD 03-JAN-2002.
XX PF 28-JUN-2001; 2001WO-US21065.
XX PR 28-JUN-2000; 2000US-0606421.
XX PR 02-AUG-2000; 2000US-0630940.
XX PR 21-AUG-2000; 2000US-0643597.
XX PR 15-SEP-2000; 2000US-0662786.
XX PR 09-OCT-2000; 2000US-0685696.
XX PR 12-DEC-2000; 2000US-0735705.
XX PR 07-MAY-2001; 2001US-0850716.
XX PA (CORI-) CORIXA CORP.
XX PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
XX PI McNeill PD, Fanger N, Retter MW, Marnierakis M, Fanger GR;
XX PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX XX
XX DR WPI; 2002-090513/12.
XX DR P-PSDB; ABB74960.
XX XX
XX PT Polynucleotides encoding lung tumor polypeptides, useful for treating
XX PT lung cancer or stimulating an immune response -
XX XX
XX PS Example 2; Page 266-267; 374pp; English.
XX XX
XX CC The present invention describes human lung tumour proteins. Human lung
XX CC tumour proteins and polynucleotides have cytostatic and immunostimulant
XX CC activities, and can be used in vaccine production. Compositions
XX CC comprising the lung tumour proteins, polynucleotides, antibodies,
XX CC fusion proteins, T cell populations, or antigen presenting cells that
XX CC express the lung tumour proteins are useful for treating lung cancer or
XX CC stimulating an immune response. ABL4959 to ABL49300 and ABB74946 to
XX CC ABB75070 represent sequences used in the exemplification of the present
XX CC invention.
XX XX
XX SQ Sequence 4181 BP; 1303 A; 830 C; 851 G; 1181 T; 16 other;
Query Match 100.0%; Score 22; DB 24; Length 4181;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 748 CTGCAAGGGGTTTGTCTGGCG 727
RESULT 15
ABA99958/c
ID ABA99958 standard; DNA; 4601 BP.
XX XX
XX AC ABA99958;

Mon Apr 21 10:29:40 2003

Search completed: April 18, 2003, 05:45:18
Job time : 100 secs

XX 05-JUL-2002 (first entry)
XX DT Human KOC DNA.
XX DE
XX KW KOC; promoter; human; cytostatic; dermatological; vulnary; tumour;
XX KW chemotherapy; allogenic bone marrow transplant; pancreatic carcinoma;
XX KW domain-containing protein overexpressed in cancer; immunostimulant;
XX KW gene therapy; chronic pancreatitis; pluripotency; aging; wound healing;
XX KW radiation therapy; skin regeneration; cell differentiation; cancer; ds.
XX OS
XX OS Homo sapiens.
XX FN WO200220036-A1.
XX PD 14-MAR-2002.
XX PF
XX PF 01-AUG-2001; 2001WO-DE02948.
XX PR 06-SEP-2000; 2000DE-1043964.
XX PR 14-FEB-2001; 2001DE-1006829.
XX XX
XX PA (MUEL/) MUELLER F.
XX XX
XX XX Mueller F, Gress T, Adler G;
XX PI
XX PI WPI; 2002-292230/33.
XX DR
XX XX
XX PT New promoter of the KOC gene, useful for diagnosis and treatment of
XX PT cancer, for inducing cellular dedifferentiation and for identifying
XX PT modulators -
XX PS
XX PS Claim 2; Fig 1a-b; 74pp; German.
XX CC
XX CC This invention describes a novel KOC (KH domain-containing protein
XX CC overexpressed in cancer) promoter. The products of the invention have
XX CC cytostatic, dermatological, vulnary and immunostimulant activity, are
XX CC capable of modulating activity/expression of the KOC protein and can be
XX CC used for gene therapy. The KOC promoter is also useful (i) for diagnosis
XX CC of tumours that express KOC, particularly for differentiating between
XX CC chronic pancreatitis and pancreatic carcinoma; (ii) to detect
XX CC premalignant lesions of uncertain nature and to classify them for risk,
XX CC and (iii) to evaluate treatments; (iv) to impart pluripotency to cells;
XX CC (v) to prepare tissues or organs (by differentiation of stem cell
XX CC populations); (vi) in high-dose chemotherapy; (vii) to improve ex vivo
XX CC expansion of hematopoietic stem cells; (viii) to improve engraftment of
XX CC allogenic bone marrow transplants; (ix) to slow down or reverse aging
XX CC processes; (x) as prophylactic agents during chemotherapy/radiation
XX CC therapy; (xi) to regenerate skin defects and accelerate wound healing,
XX CC including for cosmetic purposes; and (xii) to immunise against malignant
XX CC tumours or their precursor stages. The promoter can also be used (i) for
XX CC isolation/enrichment/selective replication of stem cells; (ii) to
XX CC determine the degree of (de)differentiation of cells and tissues; (iii)
XX CC in gene therapy of cancer (for controlling protein expression); and (iv)
XX CC to identify compounds, potentially useful in cancer treatment, that bind
XX CC to the promoter and modulate its activity. The promoter makes possible
XX CC generation of stem cells of any selected type. Since expression of KOC
XX CC is not sensitive to other physiological states, e.g. inflammation, it
XX CC represents a tumour marker with 100% sensitivity and specificity. This
XX CC sequence represents the human KOC gene described in the disclosure of
XX CC the invention.
XX SQ Sequence 4601 BP; 1462 A; 906 C; 918 G; 1298 T; 17 other;
Query Match 100.0%; Score 22; DB 24; Length 4601;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTCTGCGGCG 22
DB 1169 CTGCAAGGGGTTTCTGCGGCG 1147

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	22	100.0	1740	4	US-09-643-597-347	Sequence 347, Appl
C 2	22	100.0	4159	4	US-09-061-709-4	Sequence 4, Appli
C 3	22	100.0	4181	4	US-09-643-597-175	Sequence 175, App
C 4	16.2	73.6	5552	4	US-09-676-974-2	Sequence 2, Appli
C 5	15.6	70.9	1863	3	US-09-199-229-1	Sequence 1, Appli
C 6	15.6	70.9	1863	3	US-09-443-087-1	Sequence 1, Appli
C 7	15.6	70.9	1863	3	US-09-687-298-1	Sequence 1, Appli
C 8	15.6	70.9	3095	4	US-09-325-932A-128	Sequence 128, App
C 9	15.6	70.9	3487	4	US-09-453-702B-164	Sequence 164, App
C 10	15.6	70.9	11827	4	US-09-739-455-3	Sequence 3, Appli
C 11	15.6	70.9	48908	4	US-09-453-702B-137	Sequence 137, App
C 12	15.4	70.0	5436	2	US-08-948-277A-2	Sequence 2, Appli
C 13	15.4	70.0	5436	2	US-09-169-203-2	Sequence 2, Appli
C 14	15.2	69.1	726	4	US-09-880-116-151	Sequence 151, App
C 15	15.2	69.1	957	4	US-08-832-488-1	Sequence 1, Appli
C 16	15.2	69.1	865	3	US-09-040-483-2	Sequence 2, Appli
C 17	15.2	69.1	4208	4	US-09-214-278-6	Sequence 6, Appli
C 18	15.2	69.1	4208	4	US-09-068-740A-10	Sequence 10, Appl
C 19	15.2	69.1	5029	4	US-09-462-136-3	Sequence 3, Appli
C 20	15.2	69.1	5458	4	US-09-199-865-2	Sequence 2, Appli
C 21	15.2	69.1	5590	3	US-08-882-046-1	Sequence 1, Appli
C 22	15.2	69.1	6464	2	US-08-400-159-5	Sequence 5, Appli
C 23	15.2	69.1	6464	3	US-08-611-729A-5	Sequence 5, Appli
C 24	15.2	69.1	7130	4	US-09-056-105-31	Sequence 31, Appl
C 25	15	68.2	4368	1	US-08-026-138E-17	Sequence 17, Appl
C 26	15	68.2	4446	1	US-08-026-138E-6	Sequence 6, Appli
C 27	14.8	67.3	908	4	US-09-605-785-350	Sequence 350, App

;; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
;; FILE OF INVENTION: LUD 5538
;; FILE REFERENCE: LUD 5538
;; CURRENT APPLICATION NUMBER: US/09/061,709B
;; CURRENT FILING DATE: 1998-04-17
;; NUMBER OF SEQ ID NOS: 8
;; SEQ ID NO 4

;; LENGTH: 4159
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
US-09-061-709-4

Query Match 100.0%; Score 22; DB 4; Length 4159;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
DB 748 CTGCAAGGGGTTTGTCTGGCG 727

RESULT 3

US-09-643-597-175/c
; Sequence 175, Application US/09643597
; Patent No. 6426072

;; GENERAL INFORMATION:

;; APPLICANT: Wang, Tongtong
;; APPLICANT: Pan, Liqun
;; APPLICANT: Kalos, Michael D.
;; APPLICANT: Bangur, Chaitanya S.
;; APPLICANT: Hosken, Nancy
;; APPLICANT: Fanger, Gary R.
;; APPLICANT: Li, Samuel X.
;; APPLICANT: Wang, Aijun
;; APPLICANT: Skeiky, Yasir A.W.
;; APPLICANT: Henderson, Robert A.
;; APPLICANT: McNeill, Patricia D.

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

;; FILE REFERENCE: 210121.455C11
;; CURRENT APPLICATION NUMBER: US/09/643,597

;; CURRENT FILING DATE: 2000-08-21
;; NUMBER OF SEQ ID NOS: 369

;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 175

;; LENGTH: 4181

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: unsure

;; LOCATION: (3347)

;; OTHER INFORMATION: n=A,T,C or G

;; NAME/KEY: unsure

;; LOCATION: (3502)

;; OTHER INFORMATION: n=A,T,C or G

;; NAME/KEY: unsure

;; LOCATION: (3506)

;; OTHER INFORMATION: n=A,T,C or G

;; NAME/KEY: unsure

;; LOCATION: (3520)

;; OTHER INFORMATION: n=A,T,C or G

;; NAME/KEY: unsure

;; LOCATION: (3538)

;; OTHER INFORMATION: n=A,T,C or G

;; NAME/KEY: unsure

;; LOCATION: (3549)

;; OTHER INFORMATION: n=A,T,C or G

;; NAME/KEY: unsure

;; LOCATION: (3646)

;; OTHER INFORMATION: n=A,T,C or G

;; NAME/KEY: unsure

;; LOCATION: (3940)

;; OTHER INFORMATION: n=A,T,C or G
;; NAME/KEY: unsure
;; LOCATION: (3968)
;; OTHER INFORMATION: n=A,T,C or G
;; NAME/KEY: unsure
;; LOCATION: (3974)
;; OTHER INFORMATION: n=A,T,C or G
;; NAME/KEY: unsure
;; LOCATION: (4036)
;; OTHER INFORMATION: n=A,T,C or G
;; NAME/KEY: unsure
;; LOCATION: (4056)
;; OTHER INFORMATION: n=A,T,C or G
;; NAME/KEY: unsure
;; LOCATION: (4062)
;; OTHER INFORMATION: n=A,T,C or G
;; NAME/KEY: unsure
;; LOCATION: (4080)
;; OTHER INFORMATION: n=A,T,C or G
;; NAME/KEY: unsure
;; LOCATION: (4088)
;; OTHER INFORMATION: n=A,T,C or G
;; NAME/KEY: unsure
;; LOCATION: (4115)
;; OTHER INFORMATION: n=A,T,C or G
US-09-643-597-175

Query Match 100.0%; Score 22; DB 4; Length 4181;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
DB 748 CTGCAAGGGGTTTGTCTGGCG 727

RESULT 4

US-09-676-974-2

;; Sequence 2, Application US/09676974
;; Patent No. 6391631

;; GENERAL INFORMATION:

;; APPLICANT: HACKER, JORG
;; APPLICANT: SONNEN-BORN, ULRICH
;; APPLICANT: SCHULZE, JURGEN
;; APPLICANT: BLUM-OEHLER, GABRIELE
;; APPLICANT: MALINKA, JURGEN
;; APPLICANT: PROPERT, HANS

;; TITLE OF INVENTION: BACTERIAL PLASMIDS

;; FILE REFERENCE: 11347/268416/BET

;; CURRENT APPLICATION NUMBER: US/09/676,974

;; CURRENT FILING DATE: 2001-10-02

;; PRIOR APPLICATION NUMBER: PCT/EP98/01720

;; PRIOR FILING DATE: 1998-04-01

;; PRIOR APPLICATION NUMBER: DE 197 13543.9

;; PRIOR FILING DATE: 1997-04-02

;; NUMBER OF SEQ ID NOS: 2

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 2

;; LENGTH: 5552

;; TYPE: DNA

;; ORGANISM: Escherichia coli

;; FEATURE:

;; NAME/KEY: modified_base

;; LOCATION: (120)

;; OTHER INFORMATION: A, T, C or G

;; NAME/KEY: modified_base

;; LOCATION: (661)

;; OTHER INFORMATION: A, T, C or G

;; NAME/KEY: modified_base

;; LOCATION: (1290)

;; OTHER INFORMATION: A, T, C or G

;; NAME/KEY: modified_base

;; LOCATION: (5341)

OTHER INFORMATION: A, T, C or G
NAME/KEY: modified_base
LOCATION: (5400)
OTHER INFORMATION: A, T, C or G
US-09-676-974-2

Query Match 73.6%; Score 16.2; DB 4; Length 5552;
Best Local Similarity 85.7%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAAGGGGTTTGTCTGGCG 22
|||||
DB 1798 TCGAAGGGGTTTGTCTGGCG 1818

RESULT 5

US-09-199-229-1/c
Sequence 1, Application US/09199229
Patent No. 6063607

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie S.
APPLICANT: Berka, Randy M.
APPLICANT: Rey, Michael W.
TITLE OF INVENTION: Polypeptides Having Choline Oxidase
FILE REFERENCE: 5735.000-US
CURRENT APPLICATION NUMBER: US/09/199,229
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1863
TYPE: DNA
ORGANISM: Fusarium

US-09-199-229-1

Query Match 70.9%; Score 15.6; DB 3; Length 1863;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
DB 1359 CTGCAAGGGGCTCTGCTGGCG 1338

RESULT 6

US-09-443-087-1/c
Sequence 1, Application US/09443087
Patent No. 6146864

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie S.
APPLICANT: Berka, Randy M.
APPLICANT: Rey, Michael W.
TITLE OF INVENTION: Polypeptides Having Choline Oxidase
FILE REFERENCE: 5735.200-US
CURRENT APPLICATION NUMBER: US/09/443,087
CURRENT FILING DATE: 1999-11-18
EARLIER APPLICATION NUMBER: 09/199,229
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1863
TYPE: DNA
ORGANISM: Fusarium venenatum

US-09-443-087-1

Query Match 70.9%; Score 15.6; DB 3; Length 1863;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22

Db 1359 CTTGAAGGGGCTCTGCTGGCG 1338
|||||

RESULT 7

US-09-687-298-1/c
Sequence 1, Application US/09687298
Patent No. 6320103

GENERAL INFORMATION:

APPLICANT: Debbie Yaver
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
TITLE OF INVENTION: Polypeptides Having Choline Oxidase
FILE REFERENCE: 5735.200-US
CURRENT APPLICATION NUMBER: US/09/687,298
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 09/443,087
PRIOR FILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1863
TYPE: DNA
ORGANISM: Fusarium venenatum

US-09-687-298-1

Query Match 70.9%; Score 15.6; DB 4; Length 1863;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
DB 1359 CTTGAAGGGGCTCTGCTGGCG 1338

RESULT 8

US-09-325-932A-128/c
Sequence 128, Application US/09325932A
Patent No. 6451604

GENERAL INFORMATION:

APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
death and their use in the modification of forestry plant develop
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 128
LENGTH: 3095
TYPE: DNA
ORGANISM: Pinus radiata

US-09-325-932A-128

Query Match 70.9%; Score 15.6; DB 4; Length 3095;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
DB 2984 CTCCAGGGGTTTTCAGGGCG 2963

RESULT 9

US-09-453-702B-164/c
Sequence 164, Application US/09453702B
Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.

Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 3487
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-453-702B-164

Query Match 70.9%; Score 15.6; DB 4; Length 3487;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 1644 CTGGAAGTGGTTTGTCTGCTCG 1623

RESULT 10
US-09-739-455-3/c
Sequence 3, Application US/09739455
Patent No. 6413756
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000653
CURRENT APPLICATION NUMBER: US/09/739,455
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 11827
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(11827)
OTHER INFORMATION: n = A,T,C or G
US-09-739-455-3

Query Match 70.9%; Score 15.6; DB 4; Length 11827;
Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 10677 CTGCTGGGGTGTCTGTGAGCG 10656

RESULT 11
US-09-453-702B-137
Sequence 137, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 48908
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 137:
US-09-453-702B-137

Query Match 70.9%; Score 15.6; DB 4; Length 48908;
Best Local Similarity 81.8%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 18224 CTGGATGGGTTTGTCTGGCG 18245

RESULT 12
US-08-948-277A-2
Sequence 2, Application US/08948277A
Patent No. 5849581
GENERAL INFORMATION:
APPLICANT: Anaral, M. Catherine
Zhang, Ning

APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: Regulators of UCP3 Gene Expression
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,277A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5436 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-948-277A-2
Query Match 70.0%; Score 15.4; DB 2; Length 5436;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGGCT 17
DB 4007 CTGCAAGGGGATTGTCT 4023
RESULT 13
US-09-169-203-2
Sequence 2, Application US/09169203
Patent No. 5976808
GENERAL INFORMATION:
APPLICANT: Amaral, M. Catherine
APPLICANT: Zhang, Ning
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: Regulators of UCP3 Gene Expression
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,203
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/948,277
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5436 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-169-203-2
Query Match 70.0%; Score 15.4; DB 2; Length 5436;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTGCAAGGGGTTTGGCT 17
DB 4007 CTGCAAGGGGATTGTCT 4023
RESULT 14
US-09-280-116-151/c
Sequence 151, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 151
LENGTH: 726
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: trypsin-like serine proteases
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(726)
OTHER INFORMATION: n = a, t, c or g
US-09-280-116-151
Query Match 69.1%; Score 15.2; DB 4; Length 726;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TCGAAGGGGTTTGTGGGC 21
DB 615 TCGAAGGGGTTTGCAGGCC 596
RESULT 15
US-08-832-488-1
Sequence 1, Application US/08832488
Patent No. 6448044
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: LI, HAODONG
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: HUMAN NATURAL KILLER CELL ACTIVATION
TITLE OF INVENTION: FACTOR II
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE

us-09-270-437d-10.rni

CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,488
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF266
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 82..756
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 82..130
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 133..756
US-08-832-488-1

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Query Match      69.1%; Score 15.2; DB 4; Length 857;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 595 TGGAAAGCGGTTTTCCTGGAC 614

Search completed: April 18, 2003, 07:34:23
Job time : 32.5 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:31 ; Search time 91.3333 Seconds
(without alignments)
241.975 Million cell updates/sec

Title: US-09-270-437D-10

Perfect score: 22

Sequence: 1 ctgcaagggttttctgctggcg 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 639749 seqs, 502280378 residues

Total number of hits satisfying chosen parameters: 1279498

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	22	100.0	282	10	US-09-864-761-32671
C 2	22	100.0	588	10	US-09-864-761-16177
C 3	22	100.0	1740	10	US-09-735-705-347
C 4	22	100.0	1740	10	US-09-850-716A-347
C 5	22	100.0	1740	10	US-09-897-778-347
C 6	22	100.0	1743	10	US-09-897-778-447
C 7	22	100.0	1743	10	US-09-897-778-450
C 8	22	100.0	1764	10	US-09-850-716A-428
C 9	22	100.0	1764	10	US-09-897-778-428
C 10	22	100.0	4159	10	US-09-899-651-4
C 11	22	100.0	4181	10	US-09-735-705-175
C 12	22	100.0	4181	10	US-09-954-456-715
C 13	22	100.0	4181	10	US-09-850-716A-175
C 14	22	100.0	4181	10	US-09-897-778-175
C 15	17.2	78.2	302250	10	US-09-962-832-154
C 16	16.8	76.4	549	10	US-09-560-863-190
C 17	16.4	74.5	75899	10	US-09-854-883-243
C 18	16.2	73.6	296	10	US-09-294-093B-2223
C 19	16.2	73.6	368004	10	US-09-949-654-3

20	16.2	73.6	3309400	9	US-09-738-626-1	Sequence 1, Appli
21	15.8	71.8	261	10	US-09-878-574-15056	Sequence 15056, A
22	15.8	71.8	269	10	US-09-923-876-4150	Sequence 4150, Ap
23	15.8	71.8	272	10	US-09-878-574-14293	Sequence 14293, A
24	15.8	71.8	518	10	US-09-998-598-692	Sequence 692, App
25	15.8	71.8	2700	9	US-10-084-994-5	Sequence 5, Appli
C 26	15.8	71.8	3649	9	US-09-796-753-139	Sequence 139, App
C 27	15.6	70.9	377	10	US-09-867-701-2520	Sequence 2520, Ap
C 28	15.6	70.9	422	10	US-09-867-701-1470	Sequence 1470, Ap
C 29	15.6	70.9	426	9	US-09-738-626-1627	Sequence 1627, Ap
C 30	15.6	70.9	439	10	US-09-867-701-1485	Sequence 1485, Ap
C 31	15.6	70.9	454	10	US-09-867-701-5517	Sequence 5517, Ap
C 32	15.6	70.9	454	10	US-09-880-107-1265	Sequence 1265, Ap
C 33	15.6	70.9	454	10	US-09-967-768A-93	Sequence 93, Appli
C 34	15.6	70.9	747	9	US-09-738-626-2783	Sequence 2783, Ap
C 35	15.6	70.9	1455	9	US-09-738-626-1626	Sequence 1626, Ap
C 36	15.6	70.9	3487	9	US-10-114-170-164	Sequence 164, App
C 37	15.6	70.9	3489	10	US-09-815-242-7731	Sequence 7731, Ap
C 38	15.6	70.9	8522	10	US-09-817-181-3	Sequence 3, Appli
C 39	15.6	70.9	48908	9	US-10-114-170-137	Sequence 137, App
C 40	15.6	70.9	145831	10	US-09-969-708-79	Sequence 79, Appli
C 41	15.6	70.9	145831	10	US-09-954-456-2116	Sequence 2116, Ap
C 42	15.6	70.9	536165	9	US-09-939-984-1	Sequence 1, Appli
C 43	15.4	70.0	830	10	US-09-925-301-301	Sequence 301, App
C 44	15.2	69.1	163	10	US-09-833-381-687	Sequence 687, App
C 45	15.2	69.1	289	10	US-09-960-352-7109	Sequence 7109, Ap

ALIGNMENTS

RESULT 1

US-09-864-761-32671/c

; Sequence 32671, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aecomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 16177
;; LENGTH: 588
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC021876.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
US-09-864-761-16177

Query Match 100.0%; Score 22; DB 10; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 117 CTGCAAGGGGTTTGTCTGGCG 96

RESULT 3
US-09-735-705-347/c
; Sequence 347, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-705-347

Query Match 100.0%; Score 22; DB 10; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 498 CTGCAAGGGGTTTGTCTGGCG 477

RESULT 4
US-09-850-716A-347/c
; Sequence 347, Application US/09850716A
; Patent No. US20020115139A1

;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 32671
;; LENGTH: 282
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC021876.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
;; OTHER INFORMATION: SWISSPROT HIT: Q29125, EVALUE 3.20e-01
;; OTHER INFORMATION: NT HIT: U76705.1, EVALUE 0.00e+00
;; OTHER INFORMATION: EST_HUMAN HIT: BE545535.1, EVALUE 0.00e+00
US-09-864-761-32671

Query Match 100.0%; Score 22; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 97 CTGCAAGGGGTTTGTCTGGCG 76

RESULT 2
US-09-864-761-16177/c
; Sequence 16177, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347:
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-850-716A-347

Query Match 100.0%; Score 22; DB 10; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
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DB 498 CTGCAAGGGGTTTGTCTGGCG 477

RESULT 5

US-09-897-778-347/c
; Sequence 347, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-347

Query Match 100.0%; Score 22; DB 10; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
DB 498 CTGCAAGGGGTTTGTCTGGCG 477

RESULT 6

US-09-897-778-447/c
; Sequence 447, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-447

Query Match 100.0%; Score 22; DB 10; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
DB 498 CTGCAAGGGGTTTGTCTGGCG 477

RESULT 7

US-09-897-778-450/c
; Sequence 450, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 450
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-450

Query Match 100.0%; Score 22; DB 10; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||
DB 498 CTGCAAGGGGTTTGTCTGGCG 477

RESULT 8

US-09-850-716A-428/c
; Sequence 428, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A

us-09-270-437d-10.rnpb

Mon Apr 21 10:29:45 2003

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; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 428
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-850-716A-428

Query Match      100.0%; Score 22; DB 10; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
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DB 519 CTGCAAGGGGTTTGTCTGGGCG 498

RESULT 9
US-09-897-778-428/c
; Sequence 428, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 428
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-428

Query Match      100.0%; Score 22; DB 10; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
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DB 519 CTGCAAGGGGTTTGTCTGGGCG 498

RESULT 10
US-09-899-651-4/c
; Sequence 4, Application US/09899651
; Patent No. US2002011470A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 4
; LENGTH: 4159
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-4

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Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 748 CTGCAAGGGGTTTGTCTGGGCG 727

RESULT 11
US-09-735-705-175/c
; Sequence 175, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3347)
; OTHER INFORMATION: n=A, T, C or G
; NAME/KEY: unsure
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; OTHER INFORMATION: n=A, T, C or G
; NAME/KEY: unsure
; LOCATION: (3506)
; OTHER INFORMATION: n=A, T, C or G
; NAME/KEY: unsure
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; NAME/KEY: unsure
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; NAME/KEY: unsure
; LOCATION: (3968)

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OTHER INFORMATION: n=A,T,C or G
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LOCATION: (4088)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4115)
OTHER INFORMATION: n=A,T,C or G
US-09-735-705-175

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 748 CTGCAAGGGGTTTGTCTGGGCG 727

RESULT 12

US-09-954-456-715/c
Sequence 715, Application US/09954456
Patent No. US20020115057A1

GENERAL INFORMATION:

APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
PRIOR APPLICATION NUMBER: 2001-09-18
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patent version 3.0
SEQ ID NO 715
LENGTH: 4181
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: n=a,t,g or c

US-09-954-456-715

Query Match 100.0%; Score 22; DB 10; Length 4181;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGGCG 22
Db 748 CTGCAAGGGGTTTGTCTGGGCG 727

RESULT 13

US-09-850-716A-175/c
Sequence 175, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 175
LENGTH: 4181

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (3347)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3502)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3506)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3520)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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NAME/KEY: unsure
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OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3940)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3974)
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NAME/KEY: unsure
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NAME/KEY: unsure
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OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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OTHER INFORMATION: n=A,T,C or G

us-09-270-437d-10.rnpb

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; NAME/KEY: unsure
; LOCATION: (4088)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
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; OTHER INFORMATION: n=A,T,C or G
US-09-850-716A-175

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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 748 CTGCAAGGGGTTTGTCTGGCG 727

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; SEQ ID NO 154
; LENGTH: 302250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-154

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Db 91459 CTGCAAGGGGTACAGCTGGCG 91438

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RESULT 14
US-09-897-778-175/c
; Sequence 175, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3347, 3502, 3506, 3520, 3538, 3549, 3646, 3940, 3968, 3974,
; LOCATION: 4036, 4056, 4062, 4080, 4088, 4115
; OTHER INFORMATION: n = A,T,C or G
US-09-897-778-175

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Query Match      100.0%; Score 22; DB 10; Length 4181;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 748 CTGCAAGGGGTTTGTCTGGCG 727

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RESULT 15
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; Sequence 154, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25

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SUMMARIES

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C 2	22	100.0	282	33	US-09-864-761-32671 Sequence 32671, A
C 3	22	100.0	282	42	US-10-203-134-24949 Sequence 24949, A
C 4	22	100.0	282	42	US-10-203-137-25064 Sequence 25064, A
C 5	22	100.0	285	29	US-09-758-442-323 Sequence 323, App
C 6	22	100.0	285	42	US-10-217-623-323 Sequence 323, App
C 7	22	100.0	301	14	US-09-076-898-395 Sequence 395, App
C 8	22	100.0	301	14	US-09-076-898A-395 Sequence 395, App
C 9	22	100.0	301	34	US-09-912-292-11611 Sequence 11611, A
C 10	22	100.0	369	20	US-08-668-236-703 Sequence 703, App
C 11	22	100.0	369	20	US-09-534-846B-34372 Sequence 34372, A
C 12	22	100.0	404	14	US-09-076-897-1393 Sequence 1393, App
C 13	22	100.0	404	14	US-09-076-897B-1393 Sequence 1393, App
C 14	22	100.0	404	14	US-09-076-897C-1393 Sequence 1393, App
C 15	22	100.0	588	1	PCT-US01-00663-12084 Sequence 12084, A
C 16	22	100.0	588	33	US-09-864-761-16177 Sequence 16177, A
C 17	22	100.0	588	42	US-10-203-134-12077 Sequence 12077, A
C 18	22	100.0	588	42	US-10-203-137-12084 Sequence 12084, A
C 19	22	100.0	843	17	US-09-399-932-4493 Sequence 4493, App
C 20	22	100.0	1740	1	PCT-US01-47576-347 Sequence 347, App
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RESULT 2
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; Sequence 32671, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6

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; PRIOR APPLICATION NUMBER: GB 24263.6

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1 PRIOR FILING DATE: 2000-09-27
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4 PRIOR APPLICATION NUMBER: PCT/US01/006667
5 PRIOR FILING DATE: 2001-01-30
6 PRIOR APPLICATION NUMBER: PCT/US01/006664
7 PRIOR FILING DATE: 2001-01-30
8 PRIOR APPLICATION NUMBER: PCT/US01/006669
9 PRIOR FILING DATE: 2001-01-30
10 PRIOR APPLICATION NUMBER: PCT/US01/006665
11 PRIOR FILING DATE: 2001-01-30
12 PRIOR APPLICATION NUMBER: PCT/US01/006668
13 PRIOR FILING DATE: 2001-01-30
14 PRIOR APPLICATION NUMBER: PCT/US01/006663
15 PRIOR FILING DATE: 2001-01-30
16 PRIOR APPLICATION NUMBER: PCT/US01/006662
17 PRIOR FILING DATE: 2001-01-30
18 PRIOR APPLICATION NUMBER: PCT/US01/006661
19 PRIOR FILING DATE: 2001-01-30
20 PRIOR APPLICATION NUMBER: PCT/US01/006670
21 PRIOR FILING DATE: 2001-01-30
22 PRIOR APPLICATION NUMBER: US 60/234,687
23 PRIOR FILING DATE: 2000-09-21
24 PRIOR APPLICATION NUMBER: US 09/608,408
25 PRIOR FILING DATE: 2000-06-30
26 PRIOR APPLICATION NUMBER: US 09/774,203
27 PRIOR FILING DATE: 2001-01-29
28 NUMBER OF SEQ ID NOS: 49117
29 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
30 SEQ ID NO 32671
31 LENGTH: 282
32 TYPE: DNA
33 ORGANISM: Homo sapiens
34 FEATURE:
35 OTHER INFORMATION: MAP TO AC021876.2
36 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
37 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
38 OTHER INFORMATION: SWISSPROT HIT: Q29125, EVALUAE 3.20e-01
39 OTHER INFORMATION: NT HIT: U76705.1, EVALUAE 0.00e+00
40 OTHER INFORMATION: EST_HUMAN HIT: BE545535.1, EVALUAE 0.00e+00
41
42 US-09-864-761-32671

```

Query Match	100.0%;	Score 22;	DB 33;	Length 282;
Best Local Similarity	100.0%;	Pred. No. 5.4;		


```
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGCAAGGGGTTTGTGGGCG 22
Db 97 CTGCAAGGGGTTTGTGGGCG 76

RESULT 3
US-10-203-134-24949/c
; Sequence 24949, Application US/10203134
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW
; FILE REFERENCE: PB 0004 WO 6
; CURRENT APPLICATION NUMBER: US/10/203,134
; PRIOR FILING DATE: 2002-08-02
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38628
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 24949
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021876.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: Q29125, EVALUE 3.20e-01
; FEATURE:
; OTHER INFORMATION: NT HIT: U76705.1, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE545535.1, EVALUE 0.00e+00
US-10-203-134-24949
Query Match 100.0%; Score 22; DB 42; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGCAAGGGGTTTGTGGGCG 22
Db 97 CTGCAAGGGGTTTGTGGGCG 76

RESULT 4
US-10-203-137-25064/c
; Sequence 25064, Application US/10203137
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
```

```
FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: US/10/203,137
; CURRENT FILING DATE: 2002-08-02
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 25064
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021876.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; FEATURE:
; OTHER INFORMATION: SWISSPROT HIT: Q29125, EVALUE 3.20e-01
; FEATURE:
; OTHER INFORMATION: NT HIT: U76705.1, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE545535.1, EVALUE 0.00e+00
US-10-203-137-25064
Query Match 100.0%; Score 22; DB 42; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGCAAGGGGTTTGTGGGCG 22
Db 97 CTGCAAGGGGTTTGTGGGCG 76

RESULT 5
US-09-758-442-323/c
; Sequence 323, Application US/09758442
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE REFERENCE: PM031
; CURRENT APPLICATION NUMBER: US/09/758,442
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 710
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 323
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (109)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-758-442-323
Query Match 100.0%; Score 22; DB 29; Length 285;
```

Best Local Similarity 100.0%; Pred. No. 5.4; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTCTGGGCG 22
Db 155 CTGCAAGGGGTTTCTGGGCG 134

RESULT 6
US-10-217-623-323/c
Sequence 323, Application US/10217623
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM031CIN
CURRENT APPLICATION NUMBER: US/10/217,623
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 09/758,442
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 710
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 323
TYPE: DNA
LENGTH: 285
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (109)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (112)
OTHER INFORMATION: n equals a,t,g, or c
US-10-217-623-323

Query Match 100.0%; Score 22; DB 42; Length 285;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTCTGGGCG 22
Db 155 CTGCAAGGGGTTTCTGGGCG 134

RESULT 7
US-09-076-898-395/c
Sequence 395, Application US/09076898
GENERAL INFORMATION:
APPLICANT: Craig A. Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products - P031
NUMBER OF SEQUENCES: 2204
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,898
FILING DATE: May 13, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,004

FILING DATE: May 13, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: P031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 395:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-076-898-395

Query Match 100.0%; Score 22; DB 14; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTCTGGGCG 22
Db 162 CTGCAAGGGGTTTCTGGGCG 141

RESULT 8
US-09-076-898A-395/c
Sequence 395, Application US/09076898A
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A., et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 31
FILE REFERENCE: PO-31
CURRENT APPLICATION NUMBER: US/09/076,898A
CURRENT FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/047,004
PRIOR FILING DATE: 1997-05-13
NUMBER OF SEQ ID NOS: 2204
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 395
LENGTH: 301
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (6)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (115)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (118)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (261)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (263)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (264)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (284)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (289)
OTHER INFORMATION: n equals a,t,g, or c
US-09-076-898A-395

Query Match 100.0%; Score 22; DB 14; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
Db 162 CTGCAAGGGGTTTGTCTGGCG 141

RESULT 9
US-09-912-292-11611/c
; Sequence 11611, Application US/09912292
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 101
; CURRENT APPLICATION NUMBER: US/09/912,292
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 08/103,746
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 09/859,417
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 08/103,743
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 09/741,827
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/813,154
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/196,482
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 09/783,587
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 08/196,481
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 08/220,662
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 08/220,661
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 08/275,627
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/345,704
; PRIOR FILING DATE: 1994-11-21
; PRIOR APPLICATION NUMBER: 09/859,662
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 08/401,881
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: 09/782,161
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 08/790,776
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: 60/010,803
; PRIOR FILING DATE: 1996-01-30
; PRIOR APPLICATION NUMBER: 08/799,180
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: 60/011,618
; PRIOR FILING DATE: 1996-02-13
; PRIOR APPLICATION NUMBER: 08/803,609
; PRIOR FILING DATE: 1997-02-21
; PRIOR APPLICATION NUMBER: 60/011,985
; PRIOR FILING DATE: 1996-02-21
; PRIOR APPLICATION NUMBER: 08/971,050
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/031,038
; PRIOR FILING DATE: 1996-11-18
; PRIOR APPLICATION NUMBER: 08/975,985
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/031,221
; PRIOR FILING DATE: 1996-11-25
; PRIOR APPLICATION NUMBER: 08/985,366
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: 09/842,827
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/032,782
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 09/076,898
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/047,004

; PRIOR FILING DATE: 1997-05-13
; PRIOR APPLICATION NUMBER: 09/078,614
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: 60/046,498
; PRIOR FILING DATE: 1997-05-14
; PRIOR APPLICATION NUMBER: 09/189,834
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/065,454
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 09/366,690
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/095,484
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 09/342,216
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/091,171
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/342,061
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/091,170
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/487,572
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/116,678
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 09/497,772
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/118,784
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 09/504,577
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/120,434
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/517,011
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/122,447
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 09/628,857
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/145,956
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/628,858
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/145,955
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/741,033
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/773,518
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/171,621
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/796,765
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/867,682
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/187,016
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/225,269
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,629
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 55553
; SEQ ID NO 11611
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: n is equal to a.t.g, or c
; NAME/KEY: misc_feature
; LOCATION: (115)..(115)
; OTHER INFORMATION: n is equal to a.t.g, or c

us-09-270-437d-10.rnrm

Mon Apr 21 10:29:47 2003

NAME/KEY: misc feature
 LOCATION: (118)..(118)
 OTHER INFORMATION: n is equal to a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (261)..(261)
 OTHER INFORMATION: n is equal to a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (263)..(264)
 OTHER INFORMATION: n is equal to a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (284)..(284)
 OTHER INFORMATION: n is equal to a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (289)..(289)
 OTHER INFORMATION: n is equal to a,t,g, or c
 US-09-912-292-11611

Query Match 100.0%; Score 22; DB 34; Length 301;
 Best Local Similarity 100.0%; Pred. No. 5.5; 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
 DB 162 CTGCAAGGGGTTTGTCTGGCG 141

RESULT 10
 US-08-668-236-703/c
 ; Sequence 703, Application US/08668236
 ; GENERAL INFORMATION:
 ; APPLICANT: Stuart, Susan G.
 ; APPLICANT: Delegeane, Angelo M.
 ; APPLICANT: Bills, Pamela Kay
 ; APPLICANT: Pham, Mino T.
 ; APPLICANT: Altus, Christina T.
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Akersblom, Ingrid E.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM A
 ; TITLE OF INVENTION: HUMAN NEURONAL PRECURSOR CELL LINE
 ; NUMBER OF SEQUENCES: 1403
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3330 HILLVIEW AVENUE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/668,236
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: LUTHER, BARBARA J.
 ; REGISTRATION NUMBER: 33954
 ; REFERENCE/DOCKET NUMBER: PD-0038P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 855-0555
 ; TELEFAX: (415) 852-0195
 ; INFORMATION FOR SEQ ID NO: 703:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 369 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; CLONE: 268739
 US-08-668-236-703

Query Match 100.0%; Score 22; DB 10; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.7; 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0
 QY 1 CTGCAAGGGGTTTGTCTGGCG 22
 DB 150 CTGCAAGGGGTTTGTCTGGCG 129

RESULT 11
 US-09-534-846B-34372/c
 ; Sequence 34372, Application US/09534846B
 ; GENERAL INFORMATION:
 ; APPLICANT: Seilhamer, Jeffrey J.
 ; APPLICANT: Delegeane, Angelo M.
 ; APPLICANT: Stuart, Susan G.
 ; APPLICANT: Stuve, Laura L.
 ; APPLICANT: Mullahy, Sara J.
 ; APPLICANT: Naughton, Rebecca E.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING GROWTH, DEVELOPMENT, AND
 ; TITLE OF INVENTION: DIFFERENTIATION MOLECULES
 ; FILE REFERENCE: PD-1021 CIP
 ; CURRENT APPLICATION NUMBER: US/09/534,846B
 ; CURRENT FILING DATE: 2002-01-09
 ; Prior application data removed - refer to file wrapper or PALM
 ; NUMBER OF SEQ ID NOS: 38710
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 34372
 ; LENGTH: 369
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: hu00797632
 ; NAME/KEY: unsure
 ; LOCATION: 2, 78, 92, 175, 210, 271, 341
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-534-846B-34372

Query Match 100.0%; Score 22; DB 20; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.7; 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
 DB 150 CTGCAAGGGGTTTGTCTGGCG 129

RESULT 12
 US-09-076-897-1393/c
 ; Sequence 1393, Application US/09076897
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, et. al.
 ; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products - P032
 ; NUMBER OF SEQUENCES: 7180
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/076,897
 ; FILING DATE: May 13, 1998
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/047,005
FILING DATE: May 13, 1997
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PO-32
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 1393:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-076-897A-1393

Query Match 100.0%; Score 22; DB 14; Length 404;

Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||

Db 159 CTGCAAGGGGTTTGTCTGGCG 138

RESULT 13

US-09-076-897A-1393/c
Sequence 1393, Application US/09076897A
GENERAL INFORMATION:
APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products - P032
NUMBER OF SEQUENCES: 7180
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,897A
FILING DATE: May 13, 1998

CLASSIFICATION: 536

PRIOR APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: A. Anders Brookes

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PO-32

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 1393:

SEQUENCE CHARACTERISTICS:

LENGTH: 404 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-09-076-897A-1393

Query Match

Best Local Similarity 100.0%; Score 22; DB 14; Length 404;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||

Db 159 CTGCAAGGGGTTTGTCTGGCG 138

RESULT 14

US-09-076-897B-1393/c
Sequence 1393, Application US/09076897B
GENERAL INFORMATION:
APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products - P032
NUMBER OF SEQUENCES: 7180
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/076,897B

FILING DATE: May 13, 1998

CLASSIFICATION: 536

PRIOR APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: A. Anders Brookes

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PO-32

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 1393:

SEQUENCE CHARACTERISTICS:

LENGTH: 404 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-09-076-897B-1393

Query Match

Best Local Similarity 100.0%; Score 22; DB 14; Length 404;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGCG 22
|||||

Db 159 CTGCAAGGGGTTTGTCTGGCG 138

RESULT 15

US-09-076-897C-1393/c
Sequence 1393, Application US/09076897C
GENERAL INFORMATION:
APPLICANT: Rosen, Craig, et al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 32
FILE REFERENCE: PO-32
CURRENT APPLICATION NUMBER: US/09/076,897C
CURRENT FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 1997-05-13
PRIOR FILING DATE: 60/047,005
NUMBER OF SEQ ID NOS: 7180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1393

LENGTH: 404

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (122)

Mon Apr 21 10:29:47 2003

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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (123)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (124)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (290)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (331)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (333)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (341)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (365)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (392)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-076-897C-1393

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Query Match      100.0%; Score 22; DB 14; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTGCAAGGGGTTTTTGTGGGCG 22
    |||||
Db 159 CTGCAAGGGGTTTTTGTGGGCG 138

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Search completed: April 18, 2003, 09:35:41
Job time : 1212 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:28; Search time 245.167 Seconds
(without alignments)
400.770 Million cell updates/sec

Title: US-09-270-437D-10

Perfect score: 22
Sequence: 1 ctgcaagggttttctggcg 22

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5897297 seqs, 2233080881 residues

Total number of hits satisfying chosen parameters: 11794594

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Pending Patents NA New:*
- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
 - 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
 - 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
 - 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
 - 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
 - 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
 - 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3.*
 - 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
 - 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
 - 10: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
 - 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	5	US-09-270-437D-10
2	22	100.0	369	9	Sequence 10, Appl
3	22	100.0	404	6	Sequence 34372, A
4	22	100.0	1740	9	Sequence 56784, A
5	22	100.0	1740	9	Sequence 347, App
6	22	100.0	1740	9	Sequence 478, App
7	22	100.0	1743	9	Sequence 483, App
8	22	100.0	1743	9	Sequence 447, App
9	22	100.0	1764	9	Sequence 450, App
10	22	100.0	1799	9	Sequence 428, App
11	22	100.0	2137	6	Sequence 485, App
12	22	100.0	2137	6	Sequence 44307, A
13	22	100.0	3897	8	Sequence 44307, A
14	22	100.0	4060	6	Sequence 31225, A
15	22	100.0	4060	6	Sequence 44305, A
16	22	100.0	4159	5	Sequence 44305, A
17	22	100.0	4181	9	Sequence 44305, A
18	22	100.0	4181	9	Sequence 175, App
19	22	100.0	34555	9	Sequence 55, Appl
20	17.4	79.1	177251	7	Sequence 479, App
21	17.2	78.2	601	7	Sequence 15841, A
22	17.2	78.2	1663	1	Sequence 7089, Ap
					Sequence 3190, Ap

23	17.2	78.2	1795	9	US-10-144-771-2615
24	17.2	78.2	3730	11	US-60-453-135-1
25	17.2	78.2	3730	11	US-60-453-050-1
26	17.2	78.2	324604	1	PCT-US02-14597-56
27	17.2	78.2	373882	7	US-09-947-911-356
28	16.8	76.4	395	6	US-09-615-606A-15865
29	16.8	76.4	601	7	US-09-949-016-91995
30	16.8	76.4	601	7	US-09-949-016-91996
31	16.8	76.4	45755	7	US-09-949-016-15889
32	16.8	76.4	254405	7	US-09-949-016-14381
33	16.8	76.4	713680	7	US-09-949-016-14381
34	16.4	74.5	78125	7	US-09-949-016-16006
35	16.4	74.5	178256	6	US-09-948-124-62
36	16.4	74.5	15105345	5	US-09-948-128-55
37	16.2	73.6	285	6	US-09-531-113-28495
38	16.2	73.6	449	6	US-09-912-293-146413
39	16.2	73.6	500	8	US-10-375-682-237
40	16.2	73.6	553	9	US-10-314-344-11271
41	16.2	73.6	563	6	US-09-912-293-90564
42	16.2	73.6	859	6	US-09-699-652A-7
43	16.2	73.6	1226	9	US-10-144-771-18085
44	16.2	73.6	1560	9	US-10-282-122A-38395
45	16.2	73.6	2208	8	US-10-170-235-11352

ALIGNMENTS

RESULT 1

US-09-270-437D-10
; Sequence 10, Application US/09270437D
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Teang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antige
; FILE REFERENCE: LUD 5538.1
; CURRENT APPLICATION NUMBER: US/09/270,437D
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/061,709
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-270-437D-10

Query Match 100.0%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.73; 0; Mismatches 0; Gaps 0;
Matches 22; Conservative 0

QY 1 CTGCAAGGGGTTTCTGGGCG 22

Db 1 CTGCAAGGGGTTTCTGGGCG 22

RESULT 2

US-10-314-344-34372/c
; Sequence 34372, Application US/10314344
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullaby, Sara J.
; APPLICANT: Naughton, Rebecca E.

us-09-270-437d-10.rnpn

Mon Apr 21 10:29:50 2003

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; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING GROWTH, DEVELOPMENT, AND
; TITLE OF INVENTION: DIFFERENTIATION MOLECULES
; FILE REFERENCE: PD-1021-2 CON
; CURRENT APPLICATION NUMBER: US/10/314,344
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: 09/534,846
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 07/916,491
; PRIOR FILING DATE: 1992-07-17
; PRIOR APPLICATION NUMBER: 07/977,780
; PRIOR FILING DATE: 1992-11-19
; PRIOR APPLICATION NUMBER: 08/100,523
; PRIOR FILING DATE: 1993-08-03
; PRIOR APPLICATION NUMBER: 09/008,119
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 08/196,364
; PRIOR FILING DATE: 1994-02-14
; PRIOR APPLICATION NUMBER: 08/282,991
; PRIOR FILING DATE: 1994-07-28
; PRIOR APPLICATION NUMBER: 08/438,571
; PRIOR FILING DATE: 1995-05-10
; PRIOR APPLICATION NUMBER: 08/179,873
; PRIOR FILING DATE: 1994-01-11
; PRIOR APPLICATION NUMBER: 08/504,732
; PRIOR FILING DATE: 1995-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 38710
; SOFTWARE: PERL Program
; SEQ ID NO 34372
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No: hu00797632
; NAME/KEY: unsure
; LOCATION: 2, 78, 92, 175, 210, 271, 341
; OTHER INFORMATION: a, t, c, g, or other
;
US-10-314-344-34372
Query Match 100.0%; Score 22; DB 9; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGGCG 22
Db 150 CTGCAAGGGGTTTGTCTGGGCG 129

RESULT 3
US-09-912-293-56784/c
; Sequence 56784, Application US/09912293
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
; FILE REFERENCE: PO-100
; CURRENT APPLICATION NUMBER: US/09/912,293
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 08/103,744
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 09/249,651
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 08/104,507
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 08/196,363
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 09/859,490
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 08/196,362
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 08/221,623
; PRIOR FILING DATE: 1994-03-31

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; PRIOR APPLICATION NUMBER: 08/220,691
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 09/741,830
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/813,155
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 244538
; SEQ ID NO 56784
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: n is equal to a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (122)..(124)
; OTHER INFORMATION: n is equal to a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (129)..(129)
; OTHER INFORMATION: n is equal to a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (290)..(290)
; OTHER INFORMATION: n is equal to a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (331)..(331)
; OTHER INFORMATION: n is equal to a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (333)..(333)
; OTHER INFORMATION: n is equal to a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (341)..(341)
; OTHER INFORMATION: n is equal to a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (365)..(365)
; OTHER INFORMATION: n is equal to a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (392)..(392)
; OTHER INFORMATION: n is equal to a,t,g, or c
;
US-09-912-293-56784
Query Match 100.0%; Score 22; DB 6; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTGTCTGGGCG 22
Db 159 CTGCAAGGGGTTTGTCTGGGCG 138

RESULT 4
US-10-313-986-347/c
; Sequence 347, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Jiongcong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 347
; LENGTH: 1740

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-347

Query Match 100.0%; Score 22; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
DB 498 CTGCAAGGGGTTTGTCTGGGCG 477

RESULT 5

US-10-313-986-478/c
; Sequence 478, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-478

Query Match 100.0%; Score 22; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
DB 498 CTGCAAGGGGTTTGTCTGGGCG 477

RESULT 6

US-10-313-986-483/c
; Sequence 483, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 483
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Primate
US-10-313-986-483

Query Match 100.0%; Score 22; DB 9; Length 1740;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
DB 498 CTGCAAGGGGTTTGTCTGGGCG 477

RESULT 7

US-10-313-986-447/c
; Sequence 447, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-447

Query Match 100.0%; Score 22; DB 9; Length 1743;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
DB 498 CTGCAAGGGGTTTGTCTGGGCG 477

RESULT 8

US-10-313-986-450/c
; Sequence 450, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 450
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-450

Query Match 100.0%; Score 22; DB 9; Length 1743;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
DB 498 CTGCAAGGGGTTTGTCTGGGCG 477

RESULT 9

US-10-313-986-428/c
; Sequence 428, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;; FILE REFERENCE: 210121.455C19
;; CURRENT APPLICATION NUMBER: US/10/313.986
;; CURRENT FILING DATE: 2002-12-04
;; NUMBER OF SEQ ID NOS: 560
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 428
;; LENGTH: 1764
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-313-986-428

Query Match 100.0%; Score 22; DB 9; Length 1764;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTCTGGGCG 22
|||
DB 519 CTGCAAGGGGTTTCTGGGCG 498

RESULT 10
US-10-313-986-485/c
; Sequence 485, Application US/10313986
; GENERAL INFORMATION:
; APPLICANT: Poy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313.986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 485
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-986-485

Query Match 100.0%; Score 22; DB 9; Length 1799;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTCTGGGCG 22
|||
DB 517 CTGCAAGGGGTTTCTGGGCG 496

RESULT 11
US-09-724-676-44307/c
; Sequence 44307, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44307
; LENGTH: 2137
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-44307

Query Match 100.0%; Score 22; DB 6; Length 2137;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTCTGGGCG 22
|||
DB 764 CTGCAAGGGGTTTCTGGGCG 743

RESULT 12
US-09-724-676A-44307/c
; Sequence 44307, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44307
; LENGTH: 2137
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-44307

Query Match 100.0%; Score 22; DB 6; Length 2137;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTCTGGGCG 22
|||
DB 764 CTGCAAGGGGTTTCTGGGCG 743

RESULT 13
US-10-170-235-31225/c
; Sequence 31225, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 31225
; LENGTH: 3897
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-31225

Query Match 100.0%; Score 22; DB 8; Length 3897;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTCTGGGCG 22
|||
DB 334 CTGCAAGGGGTTTCTGGGCG 313

RESULT 14
US-09-724-676-44305/c
; Sequence 44305, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44305
; LENGTH: 4060
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-724-676-44305

Query Match 100.0%; Score 22; DB 6; Length 4060;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
 DB 764 CTGCAAGGGGTTTGTCTGGCG 743

RESULT 15

US-09-724-676A-44305/c
 ; Sequence 44305, Application US/09724676A
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676A
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 44305
 ; LENGTH: 4060
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-724-676A-44305

Query Match 100.0%; Score 22; DB 6; Length 4060;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGCG 22
 DB 764 CTGCAAGGGGTTTGTCTGGCG 743

Search completed: April 18, 2003, 10:03:47
 Job time : 256.167 secs


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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3456407"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
BASE COUNT      221 a 193 c 209 g 167 t
ORIGIN
Query Match      100.0%; Score 22; DB 10; Length 790;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
Db 416 CTGCAAGGGGTTTGTCTGGGCG 395

RESULT 2
BI520069/c
LOCUS      743 bp mRNA linear EST 29-AUG-2001
DEFINITION 603071386F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163429 5',
RNA sequence.
ACCESSION  BI520069.1 GI:15344861
VERSION     BI520069.1
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 743)
REFERENCE   NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS    National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M1405 row: 1 column: 22
High quality sequence start: 9
High quality sequence stop: 704.
Features
Location/Qualifiers
1..743
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5163429"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dt primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT      226 a 167 c 174 g 176 t
ORIGIN
Query Match      92.7%; Score 20.4; DB 13; Length 743;
Best Local Similarity 95.5%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RPCI-23-299D12"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      109 a 135 c 112 g 180 t
ORIGIN
Query Match      88.2%; Score 19.4; DB 17; Length 537;
Best Local Similarity 95.2%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCAAGGGGTTTGTCTGGGCG 22
|||||
Db 426 TGCAAGGGGTTTGTCTGGGCG 446

RESULT 4
BG699047/c
LOCUS      813 bp mRNA linear EST 07-MAY-2001
DEFINITION 602678681F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4811420 5',
mRNA sequence.

```

```

QY 1 CTGCAAGGGGTTTGTCTGGGCG 22
|||||
Db 268 CTGCAAGGGGTTTGTCTGGGCG 247

RESULT 3
AZ019431
LOCUS      537 bp DNA linear GSS 25-FEB-2000
DEFINITION RPCI-23-299D12.TJ RPCI-23 Mus musculus genomic clone RPCI-23-299D12
, DNA sequence.
ACCESSION  AZ019431
VERSION     AZ019431.1 GI:7094815
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 537)
REFERENCE   Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatman, S., Akinret
AUTHORS     B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
TITLE      Mouse BAC End Sequences from Library RPCI-23
JOURNAL     Unpublished (1999)
COMMENT     Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(piet@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 239 row: D column: 12
Seq primer: SP6
Class: BAC ends.
Features
Location/Qualifiers
1..537
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-299D12"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      109 a 135 c 112 g 180 t
ORIGIN
Query Match      88.2%; Score 19.4; DB 17; Length 537;
Best Local Similarity 95.2%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCAAGGGGTTTGTCTGGGCG 22
|||||
Db 426 TGCAAGGGGTTTGTCTGGGCG 446

RESULT 4
BG699047/c
LOCUS      813 bp mRNA linear EST 07-MAY-2001
DEFINITION 602678681F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4811420 5',
mRNA sequence.

```


ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 466;
 Best Local Similarity 90.9%; Pred. No. 3.3e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCAAGGGGTTTCTGGCG 22
 |||||
 Db 300 CTGCCAGGGGTTTCTGGGTG 279

RESULT 7

DR6F10S DR6F10S 615 bp DNA linear GSS 06-JUN-2002
 LOCUS DR6F10S 615 bp DNA linear GSS 06-JUN-2002
 DEFINITION Danio rerio genomic clone DKey-6F10, genomic survey sequence.

ACCESSION AL744135
 VERSION AL744135.1 GI:21354443

KEYWORDS

SOURCE zebrafish.

ORGANISM

Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 615)
 Humphray, S.J., Huckle, E. and Hunt, S.E.

REFERENCE

AUTHORS Direct Submission
 TITLE. Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
 CAMPUS, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
 humquerry@sanger.ac.uk Unpublished

JOURNAL This sequence was generated from the SP6 end of BAC 6F10. 6F10 is
 part of the Daniokey Pilot BAC Library created by R. Plasterk and
 N.V. Keygene.

COMMENT Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

1..615
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone="DKey-6F10"
 /tissue_type="Testis"
 /note="vector pindigBAC-536"

BASE COUNT 197 a 106 c 117 g 195 t

ORIGIN

Query Match 81.8%; Score 18; DB 17; Length 615;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCACGGGGTTTCTGG 19
 |||||
 Db 271 TGCACGGGGTTTCTGG 288

RESULT 8

BQ166727/c BQ166727/c 375 bp mRNA linear EST 25-APR-2002
 LOCUS BQ166727 375 bp mRNA linear EST 25-APR-2002
 DEFINITION WHE0924_D07 H442T wheat 5-15 DAP spike cDNA library Triticum
 aestivum cDNA clone WHE0924_D07_H14, mRNA sequence.

ACCESSION BQ166727

VERSION BQ166727.1 GI:20310411

KEYWORDS

SOURCE bread wheat.

ORGANISM

Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Triticum.

1 (bases 1 to 375)
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han

, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,

Seaton, C.L. and Tong, J.C.

TITLE The structure and function of the expressed portion of the wheat
 genomes - 5-15 DAP spike cDNA library

JOURNAL

COMMENT Unpublished (2000)

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: candersn@pw.usda.gov

This EST was generated by sequencing from the 3' end of the clone.
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20.

Seq primer: T7 primer.

Location/Qualifiers

1..375
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE0924_D07_H14"
 /clone_lib="Wheat 5-15 DAP spike cDNA library"
 /tissue_type="Spike"
 /dev_stage="Adult plant"
 /lab_host="E. coli SOLR"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI; Site 2: XhoI; plants were grown in the
 greenhouse. Spikes at 5, 10 and 15 DAP were harvested,
 total RNA and poly(A) RNA were prepared, a cDNA library
 was made, and the cDNA clones were in vivo excised to
 give phagescript phagemids in the T7 Clonase lab (Choi,
 Riverside, Plasmid DNA preparations and DNA sequencing
 were performed in the OD Anderson lab (all other authors
)."

BASE COUNT 91 a 110 c 81 g 93 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 14; Length 375;
 Best Local Similarity 90.5%; Pred. No. 8.7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCACGGGGTTTCTGGCG 22

Db 49 TGCACGGGGTTTCTGGGTG 29

RESULT 9

BM728827/c

LOCUS BM728827 714 bp mRNA linear EST 01-MAR-2002

DEFINITION UI-E-E01-aiv-f-19-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone

UI-E-E01-aiv-f-19-0-UI 5', mRNA sequence.

ACCESSION BM728827

VERSION BM728827.1 GI:19050160

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 714)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalisation and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

9704477

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.wesg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

IMAGE:3716837 3' similar to contains element MSRI repetitive element /, mRNA sequence.
 AT545505
 AT545505.1 GI:4462878
 EST.
 zebrafish.
 Dario rerio
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 271)
 Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T., Underwood, K., Stepcoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 WashU Zebrafish EST Project 1998
 Unpublished (1998)
 Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrafish@watson.wustl.edu
 cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone Distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and ResourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
 Seq primer: T7 ET from Amersham
 High quality sequence stop: 269
 POLYA=No.

Location/Qualifiers
 1. .271
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone="IMAGE:3716837"
 /clone_lib="Zebrafish WashU MPIMG EST"
 /sex="mixed"
 /tissue_types="26 somite embryos, adult livers, shield stage embryos"
 /lab_host="X11-blue MRF"
 /note=vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'-pGACTGTTTCAGTTCGAGCGCGCCCTTTTCTTTTCTTTT3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

BASE COUNT 31 a 50 c 63 g 127 t
 ORIGIN

Query Match 79.1%; Score 17.4; DB 9; Length 271;
 Best Local Similarity 94.7%; Pred No. 1.2e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ov 4 CAAGGGGTTTGTGGCG 22

JOURNAL
COMMENT

Gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@anri.barc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGTACGACG
Plate: 108 row: H column: 3
Seq primer: ATTAGGTGACACTATAG.

FEATURES
source

1..556
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC SBOV"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

BASE COUNT 166 a 94 c 111 g 185 t
ORIGIN

Query Match 79.1%; Score 17.4; DB 12; Length 556;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCAGGGGTTTGTCTGGG 20
|||||
Db 320 TGCAGGGGTTTGTCTGTG 338

RESULT 15
BE899763
LOCUS

DEFINITION 202763 MARC 2BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001
ACCESSION BE899763
VERSION BE899763.1 GI:10387237
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 573)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W., Rohrer,G.A., Chitko-McKown,C.G.,
Pertea,G., Holt,I., Karamycheva,S., Liang,P., Quackenbush,J. and
Keefe,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGTACGACG

Plate: 42 row: G column: 17
Seq primer: ATTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1..573

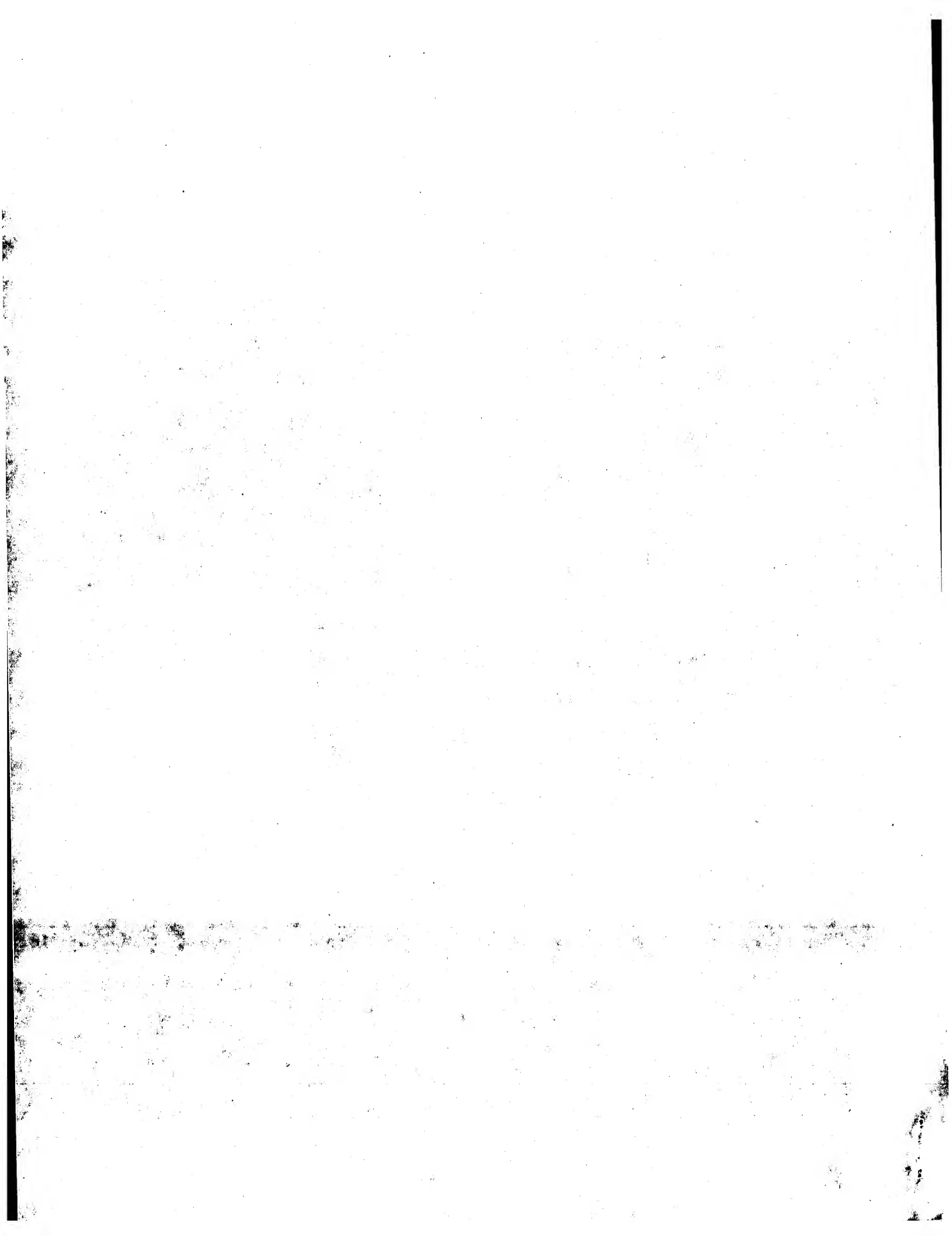
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 165 a 97 c 112 g 199 t
ORIGIN

Query Match 79.1%; Score 17.4; DB 12; Length 573;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCAGGGGTTTGTCTGGG 20
|||||
Db 311 TGCAGGGGTTTGTCTGTG 329

Search completed: April 18, 2003, 07:31:49
Job time : 771.167 secs



GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:46:26 ; Search time 292 Seconds
(without alignments)
2192.677 Million cell updates/sec

Title: US-09-270-437D-11

Perfect score: 22
Sequence: 1 tcttgcgcgcgtgcgcctcag 22

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.ey.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	22	100.0	1946	6	AR171866	AR171866 Sequence
C 2	22	100.0	147767	2	AC105030	AC105030 Homo sapi
C 3	22	100.0	168613	9	AC091133	AC091133 Homo sapi
C 4	18.8	85.5	12110	1	AE001245	AE001245 Treponema
C 5	18.8	85.5	175585	2	AC118983	AC118983 Rattus no
C 6	17.8	80.9	2023	9	AF463492	AF463492 Homo sapi
C 7	17.8	80.9	2082	9	AK027725	AK027725 Homo sapi
C 8	17.8	80.9	2477	9	BC026308	BC026308 Homo sapi
C 9	17.8	80.9	146180	9	AC007193	AC007193 Homo sapi
C 10	17.8	80.9	210868	2	AC099392	AC099392 Rattus no
C 11	17.4	79.1	352	11	R1CGL48A	D14746 Oryza sativ
C 12	17.4	79.1	7419	9	AB061849	AB061849 Homo sapi
C 13	17.4	79.1	83052	2	CNS08C9Y	AL772420 Oryza sat
C 14	17.4	79.1	132592	2	AL589792	AL589792 Homo sapi
C 15	17.4	79.1	166518	9	HS120G22	AL031847 Human DNA
C 16	17.4	79.1	173627	9	AC004963	AC004963 Homo sapi
C 17	17.2	78.2	552	3	AF153349	AF153349 Leishmani
C 18	17.2	78.2	818	9	HS336031	AF153349 Leishmani
C 19	17.2	78.2	888	9	HUM21SEQJ	AJ336031 Homo sapi
C 20	17.2	78.2	1426	3	AY069730	M97565 Human (Clon
C 21	17.2	78.2	1686	10	BC030347	AY069730 Drosophill
C 22	17.2	78.2	1727	10	AF214013	BC030347 Mus muscu
C 23	17.2	78.2	2719	1	AF051693	AF214013 Mus muscu
C 24	17.2	78.2	10757	1	AE004561	AF051693 Pseudomon
C 25	17.2	78.2	10981	1	AE005890	AE004561 Pseudomon
C 26	17.2	78.2	15000	3	LMFL2267	AE005890 Caulobact
C 27	17.2	78.2	15267	3	AB055099	AL357593 Leishmani
C 28	17.2	78.2	22990	3	AB055101	AB055099 Drosophill
C 29	17.2	78.2	23007	3	AB055100	AB055101 Drosophill
C 30	17.2	78.2	23244	3	AB055098	AB055100 Drosophill
C 31	17.2	78.2	61204	2	AC017132	AB055098 Drosophill
C 32	17.2	78.2	74169	2	AC128268	AC017132 Drosophill
C 33	17.2	78.2	83582	2	AC121741	AC128268 Rattus no
C 34	17.2	78.2	100499	9	AL138769	AC121741 Rattus no
C 35	17.2	78.2	102818	9	AC003042	AL138769 Human DNA
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C 37	17.2	78.2	141877	10	AL669836	Continuation (8 of
C 38	17.2	78.2	161601	3	AC007594	AL669836 Mouse DNA
C 39	17.2	78.2	163386	9	AC015723	AC007594 Drosophill
C 40	17.2	78.2	171110	2	AC096216	AC015723 Homo sapi
C 41	17.2	78.2	171537	2	AC129925	AC096216 Rattus no
C 42	17.2	78.2	177564	2	AC119477	AC129925 Homo sapi
C 43	17.2	78.2	182381	2	AC096410	AC119477 Rattus no
C 44	17.2	78.2	197406	2	AC110594	AC096410 Rattus no
C 45	17.2	78.2	200158	2	AC116771	AC110594 Homo sapi
						AC116771 Mus muscu

ALIGNMENTS

RESULT 1	AR171866	Sequence 7 from patent US 6297364.	DNA	linear	PAT 17-DEC-2001
LOCUS	AR171866	1946 bp			
DEFINITION	Sequence 7 from patent US 6297364.				
ACCESSION	AR171866				
VERSION	AR171866.1	GI:17910816			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1946)				
AUTHORS	Chen,Y.-T., Gure,A., Teang,S., Stockert,E., Jager,E., Alexander,K. and Old,L.J.				
TITLE	Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof				

Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K.,
Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,
Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K.,
Lamarez, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., McPeeters, R., Meldrum, J., Meneus, L.,
Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,
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Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE JOURNAL

Submitted (01-APR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamarez, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J.,
Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE JOURNAL

Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE AUTHORS

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
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Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
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O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
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Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

TITLE JOURNAL

Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Jul 1, 2002 this sequence version replaced gi:21431160.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: LI2028
Center clone name: 501_C14

FEATURES

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unsure	484..488 /note="<30 qual SNGL region"
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unsure	1293..1296 /note="<30 quality SNGL region"
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repeat_region	complement(4318..4415) /rpt_family="U6"
repeat_region	5302..5438 /rpt_family="MIR"
repeat_region	complement(5443..5828) /rpt_family="LIM4"
repeat_region	complement(6003..6309) /rpt_family="AluJb"
repeat_region	6349..6651 /rpt_family="AluSg"
repeat_region	6666..6941 /rpt_family="AluJo"
repeat_region	7125..7447 /rpt_family="AluSx"
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[illegible]

clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 32 Row: j Column: 19

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11968004.

FEATURES

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Query Match	Score 17.8;	DB 9;	Length 2477;
Best Local Similarity	90.5%;	Pred. No. 3.9e+03;	
Matches 19;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;

RESULT 9
AC007193/c

AC007193 146180 bp DNA linear PRI 17-JUN-1999
AC007193/c Homo sapiens chromosome 19, BAC 82621 (CIT-B-139a18), complete
LOCUS sequence.
DEFINITION
AC007193 AC007193
AC007193 AC007193
AC007193.1 GI:4558635
HTG.
Homo sapiens.
Homo sapiens.
Homo sapiens.
ORGANISM
SOURCE
Chordata: Craniata: Vertebrata: Euteleostomi;

REFERENCE
AUTHORS

AUTHORS

Lamerdin, J. B., McCreedy, Gordon, L., Dias, J., Ramirez, M., Burkhardt-Schulz, K. J., Gordon, L., Velasco, N., Do, L., Regala, M., Terry, A., Stillwagen, S., Phan, H., Velasco, N., Christensen, M., Georgescu, A., Garsen, J., Danganan, L., Erlar, A., Andreise, I., Trankheim, M., Avila, J., Liu, S., Attix, C., Duarte, S., Lucas, S., Bruce, R., Ow, D., Amico-Keller, G., Coefield, J., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Sanders, C. V., Thomas, P., Trong, S., Kobayashi, A., Olsen, A. S. and Carrano, A. V.

TITLE

Sequence analysis of a 1.9 Mb region in 19ql3.2 between APOE and D19S412

**JOURNAL
REFERENCE**

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
2	(bases 1 to 146180)	Lamerdin, J.E.	Direct Submission	
	Submitted (02-APR-1999)	Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA		
	(CIT-B-139a18)	overlaps BAC 284575 (CIT-B-297n14) to the left from		
	bases 1 to 27,487 of this accession, and separated from BAC 89581			
	(CIT-B-158d10)	on the right by a gap of approximately 17 to 23 kb		
	Additional chromosome 19 map and sequence information may be			
	found at http://www-bio.llnl.gov/bbrp/genome/genome.html .			

FEATURES

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Best Local Similarity 90.5%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTTTGGCGCTGCGGCCTCAG 22
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RESULT 10 210868 bp DNA linear HTG 17-JUN-2002
LOCUS Rattus norvegicus clone CH230-160L8, *** SEQUENCING IN PROGRESS
DEFINITION Rattus norvegicus pieces.
ACCESSION AC099392
VERSION AC099392.6 GI:21744099
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
1 (bases 1 to 210868)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Allbrooks,S.L., Anaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbarta,J.J., Benton,J., Binnage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhaq,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleaveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hennings,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homai,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
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Kratochiv,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Litcharge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mashiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Mosher,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokwenwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,

Mon Apr 21 10:29:54 2003

Peters, L., Dickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojokan, I., Rolfe, M., Ruiz, S., Savary, G.,
 Scherer, S., Scott, G., Shen, H., Shoohart, N., Sisson, I.,
 Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Uman, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wlezyk, R., Woodson, S., Worley, K.,
 Wu, C., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 210868)
 Worley, K.C.
 Submitted (10-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 210868)
 Worley, K.C.
 Direct Submission
 Submitted (17-JUN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 13, 2002 this sequence version replaced gi:18700960.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GKZE
 Center clone name: CH230-160L8
 ----- Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 147538 bases at least Q40
 Consensus quality: 152247 bases at least Q30
 Consensus quality: 155330 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 69 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 1434: contig of 1434 bp in length
 * 1435 1534: gap of unknown length
 * 1535 2658: contig of 1124 bp in length
 * 2659 2759: gap of unknown length
 * 2759 4174: contig of 1416 bp in length
 * 4175 4274: gap of unknown length
 * 4275 5456: contig of 1182 bp in length
 * 5457 5556: gap of unknown length
 * 5557 6845: contig of 1289 bp in length
 * 6846 6945: gap of unknown length
 * 6946 8314: contig of 1368 bp in length
 * 8314 8414: gap of unknown length
 * 8414 9593: contig of 1080 bp in length
 * 9593 9594: gap of unknown length
 * 9594 11067: contig of 1473 bp in length
 * 11067 12215: gap of unknown length
 * 12215 12316: contig of 1049 bp in length
 * 12316 13612: contig of 1297 bp in length
 * 13612 13713: gap of unknown length
 * 13713 15322: contig of 1610 bp in length
 * 15322 15333: gap of unknown length
 * 15333 15422: gap of unknown length
 * 15422 15433: contig of 1251 bp in length
 * 15433 16674: gap of unknown length
 * 16674 18285: contig of 1512 bp in length
 * 18285 18385: gap of unknown length
 * 18385 19363: contig of 1250 bp in length
 * 19363 21369: gap of unknown length
 * 21369 21469: contig of 1634 bp in length
 * 21469 22777: gap of unknown length
 * 22777 24514: gap of unknown length
 * 24514 26098: contig of 1637 bp in length
 * 26098 26198: gap of unknown length
 * 26198 28120: contig of 1484 bp in length
 * 28120 28221: gap of unknown length
 * 28221 29582: contig of 1922 bp in length
 * 29582 30966: gap of unknown length
 * 30966 32439: contig of 1383 bp in length
 * 32439 32440: gap of unknown length
 * 32440 34540: contig of 1374 bp in length
 * 34540 34742: contig of 2102 bp in length
 * 34742 35939: gap of unknown length
 * 35939 36039: contig of 1198 bp in length
 * 36039 36040: gap of unknown length
 * 36040 37281: contig of 1241 bp in length
 * 37281 37380: gap of unknown length
 * 37380 40008: contig of 1262 bp in length
 * 40008 40108: gap of unknown length
 * 40108 42626: contig of 2628 bp in length
 * 42626 42727: gap of unknown length
 * 42727 44807: contig of 2518 bp in length
 * 44807 44907: gap of unknown length
 * 44907 46287: contig of 2081 bp in length
 * 46287 46388: gap of unknown length
 * 46388 48246: contig of 1380 bp in length
 * 48246 48347: gap of unknown length
 * 48347 50359: contig of 1859 bp in length
 * 50359 50459: gap of unknown length
 * 50459 51749: contig of 2013 bp in length
 * 51749 51849: gap of unknown length
 * 51849 53917: contig of 1290 bp in length
 * 53917 54017: gap of unknown length
 * 54017 56174: contig of 2068 bp in length
 * 56174 56273: gap of unknown length
 * 56273 58609: contig of 2156 bp in length
 * 58609 58709: gap of unknown length
 * 58709 61307: contig of 2336 bp in length
 * 61307 61407: gap of unknown length
 * 61407 62553: contig of 2598 bp in length
 * 62553 62654: contig of 1146 bp in length
 * 62654 65586: gap of unknown length
 * 65586 67723: contig of 2933 bp in length
 * 67723 67824: gap of unknown length
 * 67824 69706: contig of 2037 bp in length
 * 69706 69807: contig of 1883 bp in length
 * 69807 72012: gap of unknown length
 * 72012 72113: contig of 2206 bp in length
 * 72113 73724: gap of unknown length
 * 73724 76122: contig of 1611 bp in length
 * 76122 76222: gap of unknown length
 * 76222 78579: contig of 2299 bp in length
 * 78579 78679: gap of unknown length
 * 78679 82740: contig of 2357 bp in length
 * 82740 82839: gap of unknown length
 * 82839 86480: contig of 4060 bp in length
 * 86480 86481: gap of unknown length
 * 86481 89433: contig of 3541 bp in length
 * 89433 89533: gap of unknown length
 * 89533 89434: contig of 2953 bp in length
 * 89434 89533: gap of unknown length

COMMENT

```

* 89534 92623: contig of 3090 bp in length
* 92624 92723: gap of unknown length
* 92724 96987: contig of 4264 bp in length
* 96988 97087: gap of unknown length
* 97088 98133: contig of 2046 bp in length
* 98134 99233: gap of unknown length
* 99234 103909: contig of 4676 bp in length
* 103910 104009: gap of unknown length
* 104010 108102: contig of 4093 bp in length
* 108103 108202: gap of unknown length
* 108203 110791: contig of 2589 bp in length
* 110792 110891: gap of unknown length
* 110892 113718: contig of 2827 bp in length

Query Match      80.9%; Score 17.8; DB 2; Length 210868;
Best Local Similarity 90.5%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2;

QY 1 TCCTTGGCGCTGCGGCTCA 21
Db 27677 TCCTTACGTGCTGCGGCTCA 27697

RESULT 11
LOCUS RICG148A/c
DEFINITION Oryza sativa (japonica cultivar-group) 352 bp DNA linear STS 29-MAY-2002
RFLP marker, clone G148, sequence tagged site.
ACCESSION D14746
VERSION D14746.1 GI:287311
KEYWORDS STS; RFLP marker; restriction fragment length polymorphism.
SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE 1 (bases 1 to 352)
AUTHORS Minobe,Y.
TITLE Nucleotide sequence of Sequence Tagged Site from rice RFLP marker
probe
JOURNAL Unpublished
COMMENT PROJECT = 'RGP'.
FEATURES
    Location/Qualifiers
        1..352
            /organism="Oryza sativa (japonica cultivar-group)"
            /cultivar="Nipponbare"
            /db_xref="taxon:39947"
            /chromosome="12"
BASE COUNT 63 a 63 c 109 g 117 t
ORIGIN

Query Match      79.1%; Score 17.4; DB 11; Length 352;
Best Local Similarity 94.7%; Pred. No. 1e+04; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 1;

QY 1 TCCTTGGCGCTGCGGCTCT 19
Db 315 TCCTTGGCGCTGCTGCTCT 297

RESULT 12
LOCUS AB061849
DEFINITION Homo sapiens RPL22 gene for ribosomal protein L22, exons 1, 2 and partial cds.
ACCESSION AB061849
VERSION AB061849.1 GI:17932991
KEYWORDS Homo sapiens DNA, clone lib:Keio BAC library.
SOURCE Homo sapiens
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

```

Yoshihama, M., Uechi, T., Asakawa, S., Kawasaki, K., Kato, S., Higa, S.,
Maeda, N., Minoshima, S., Tanaka, T., Shimizu, N. and Kenmochi, N.,
The human ribosomal protein genes: sequencing and comparative
analysis of 73 genes
Genome Res. 12 (3), 379-390 (2002)

JOURNAL 21864036
MEDLINE 2 (bases 1 to 7419)
REFERENCE Kenmochi, N. and Shimizu, N.
Direct Submission
AUTHORS Submitted (17-MAY-2001) Naoya Kenmochi, Miyazaki Medical College,
JOURNAL Central Research Laboratories, 5200 Kihara, Kiyosake, Miyazaki
889-1692 Japan (E-mail:kenmochi@post.miyazaki-med.ac.jp.
Tel:81-985-85-9665, Fax:81-985-85-1514)

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FEATURES
    source
        1..7419
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="1"
            /map="lp36.3-p36.2"
            /clone_lib="Keio BAC library"
            85..187
                /rpt_family="MER5A"
                complement(229..298)
                /rpt_family="L2"
                repeat_region
            302..386
                complement(302..386)
                /rpt_family="L2"
            816..7419
                /genes="RPL22"
            816..850
                /genes="RPL22"
            /number=1
            join(839..850,2657..>2761)
            /genes="RPL22"
            /codon_start=1
            /product="ribosomal protein L22"
            /protein_id="BAB79487.1"
            /db_xref="GI:17932992"
            /translation="MAPVKLVVKGKKKKQVLKFTLDCTHPVEDGIMDAANP"
            851..2656
                /genes="RPL22"
            /number=1
            2657..2761
                /genes="RPL22"
            /number=2
            2762..7419
                /genes="RPL22"
            /number=2
            3084..3383
                /rpt_family="AluSg"
                complement(4321..4632)
                /rpt_family="AluSp"
                complement(4634..4945)
                /rpt_family="AluSx"
                complement(4949..5249)
                /rpt_family="AluY"
                complement(5255..5519)
                /rpt_family="AluY"
                complement(5520..5808)
                /rpt_family="AluJo"
                complement(5932..6028)
                /rpt_family="MIR3"
                complement(6187..6471)
                /rpt_family="AluJb"
                6663..6791
                /rpt_family="AluJb"
                6792..7089
                /rpt_family="AluSp"
                7090..7267
                /rpt_family="AluJb"
                1705 a 1683 c 1882 g 2149 t
BASE COUNT 1705 a 1683 c 1882 g 2149 t
ORIGIN

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Query Match

79.1%; Score 17.4; DB 9; Length 7419;


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/db_xref="taxon:9606"
/chromosome="1"
/map="p36.21-36.33"
/clone="RPS-889P23"
/clone_lib="RPCI-5"
1..3331
/note="assembly_fragment:00799"
3432..90998
/note="assembly_fragment:02114"
91099..130106
/note="assembly_fragment:03033.0"
130207..132592
/note="assembly_fragment:03380"
26843 a 36833 c 36775 g 31841 t 300 others
ORIGIN

Query Match
Best Local Similarity 94.78; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCTTGGCGCTGGCGCTTC 20
Db 110808 CCTTGGCGCTGGCGCTTC 110826

RESULT 15
HS120G22 166518 bp DNA linear PRI 21-JUL-2000
LOCUS Human DNA sequence from clone RPI-120G22 on chromosome
DEFINITION AL031847
VERSION 1
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166518)
Wray, P.
Direct Submission
Submitted (20-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jul 22, 2000 this sequence version replaced gi:9368784.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/c_elegans/wormpep/
This sequence was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RPI-120G22 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
VECTOR: pcypac2
IMPORTANT: This sequence is not the entire insert of clone
RPI-120G22. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RPI-120G22 is at 166518 in this
sequence. The true left end of clone RPS-889P23 is at 90508 in this
sequence. The true right end of clone RPI-20208 is at 100 in this
sequence.

FEATURES
Source
Location/Qualifiers
1..166518
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/db_xref="taxon:9606"
/chromosome="1"
/map="p36.21-36.33"
/clone="RPI-120G22"
/clone_lib="RPCI-1"
8814..9131
/note="match: GSS: Em:AQ716455"
8816..9229
/note="match: GSS: Em:AQ239786"
10012..10541
/note="match: GSS: Em:AQ678815"
18389..18823
/note="match: GSS: Em:AQ270793"
25588..26045
/note="match: GSS: Em:AQ214655"
25694..25967
/note="match: GSS: Em:AQ097494"
complement(41087..41505)
/note="match: GSS: Em:AQ213363"
complement(41123..41505)
/note="match: GSS: Em:AQ133445"
45297..45591
/note="match: GSS: Em:AF046498"
49180..49534
/note="match: GSS: Em:AF046498"
/note="Single clone region. short insert library only"
complement(57981..58764)
/note="match: GSS: Em:AF158011"
complement(60582..61043)
/note="match: GSS: Em:AQ695221"
64797..64841
/note="Single clone region. short insert library only"
68250..68620
/note="match: STS: Em:G16281"
70460..70622
/note="match: STS: Em:G21080"
complement(74554..74895)
/note="match: GSS: Em:AQ097224"
complement(79470..79747)
/note="match: STS: Em:AF191963"
complement(79556..79740)
/note="match: GSS: Em:AQ541496"
complement(79935..80319)
/note="match: STS: Em:HSA052WG1"
complement(85942..86372)
/note="match: STS: Em:G22706"
complement(86963..87322)
/note="match: GSS: Em:AQ191756"
87339..87808
/note="match: GSS: Em:AQ698012"
88780..89285
/note="match: GSS: Em:AQ121434"
94030..94434
/note="match: GSS: Em:B89150"
94030..94405
/note="match: GSS: Em:AQ008338"
94054..94464
/note="match: GSS: Em:AQ010380"
join(112106..112211,116809..116933,123047..123132)
/note="match: GSS: Em:AQ634365"
complement(join(112121..112215,116809..116936))
/note="match: GSS: Em:AQ202845"
112126..112224
/note="match: GSS: Em:AF046385"
join(112145..112211,116809..116936)
/note="match: GSS: Em:AQ634370"
complement(join(112150..112211,116809..116933,
123047..123172))

```

us-09-270-437d-11.rge

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```

/misc_feature /note="match: GSS: Em:AQ489599"
complement(113100..113712)
/misc_feature /note="match: GSS: Em:AQ477048"
complement(113175..113715)
/misc_feature /note="match: GSS: Em:AQ476615"
113710..114090
/misc_feature /note="match: GSS: Em:AQ434236"
join(116809..116933,123047..123119)
/misc_feature /note="match: GSS: Em:AQ732842"
116809..116941
/misc_feature /note="match: GSS: Em:AQ357462"
116909..116936
/misc_feature /note="match: GSS: Em:AQ047297 Em:AQ351276"
join(116840..116933,123047..123191)
/misc_feature /note="match: STS: Em:G13224 Em:G13474"
121507..121762
/misc_feature /note="match: GSS: Em:AQ482227"
complement(123035..123248)
/misc_feature /note="match: GSS: Em:AQ779080"
123142..123248
/misc_feature /note="match: GSS: Em:AQ634365"
123192..123356
/misc_feature /note="match: STS: Em:G11177"
124453..124584
/misc_feature /note="match: GSS: Em:AQ002260"
complement(124491..124832)
/misc_feature /note="match: STS: Em:G06939"
129943..130018
/misc_feature /note="single clone region"
144105..144499
/misc_feature /note="match: GSS: Em:AQ231959"
144105..144483
/misc_feature /note="match: GSS: Em:AQ231956"
complement(148672..149104)
/misc_feature /note="match: GSS: Em:AQ672446"
152031..152510
/misc_feature /note="match: GSS: Em:AQ234353"
152031..152510
BASE COUNT 34311 a 45982 c 47124 g 39101 t
ORIGIN
Query Match 79.1%; Score 17.4; DB 9; Length 166518;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CCTTGGCGCTGCGGCTC 20
Db 110222 CCTTGGCGCTGCGGCTC 110240

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Search completed: April 18, 2003, 06:20:58
Job time : 508 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:12:35 ; Search time 98 Seconds
(without alignments)
505.551 Million cell updates/sec

Title: US-09-270-437D-11

Perfect score: 22

Sequence: 1 tccttgcgcgtcgccctcag 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Databases :

1: /SID22/gcgdata/geneseq/geneq-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneq/geneq-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneq/geneq-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneq/geneq-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneq/geneq-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneq/geneq-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneq/geneq-emb1/NA1986.DAT.*
8: /SID22/gcgdata/geneq/geneq-emb1/NA1987.DAT.*
9: /SID22/gcgdata/geneq/geneq-emb1/NA1988.DAT.*
10: /SID22/gcgdata/geneq/geneq-emb1/NA1989.DAT.*
11: /SID22/gcgdata/geneq/geneq-emb1/NA1990.DAT.*
12: /SID22/gcgdata/geneq/geneq-emb1/NA1991.DAT.*
13: /SID22/gcgdata/geneq/geneq-emb1/NA1992.DAT.*
14: /SID22/gcgdata/geneq/geneq-emb1/NA1993.DAT.*
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22: /SID22/gcgdata/geneq/geneq-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneq/geneq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneq/geneq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	21	AAZ36157
2	22	100.0	1945	21	AAZ36153
3	17.8	80.9	139	21	AAZ37338
4	17.8	80.9	1711	22	AAH07034
5	17.8	80.9	1785	23	AAH08110
6	17.8	80.9	1785	23	AAH073402
7	17.8	80.9	2082	22	AAH14706
8	17.2	78.2	464	22	AAH63986
9	17.2	78.2	1217	23	ABL29179

C	10	17.2	78.2	3408	23	ABL29178	Drosophila melanog
C	11	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	12	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	13	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	14	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	15	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	16	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	17	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	18	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	19	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	20	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	21	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	22	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	23	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	24	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	25	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	26	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	27	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	28	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	29	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	30	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	31	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	32	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	33	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	34	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	35	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	36	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	37	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	38	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	39	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	40	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	41	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	42	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	43	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	44	16.8	76.4	462	22	AAZ36157	Human breast cancer
C	45	16.8	76.4	462	22	AAZ36157	Human breast cancer

ALIGNMENTS

RESULT 1
AAZ36157
ID AAZ36157 standard; DNA; 22 BP.
XX
AC AAZ36157;
XX

DT 11-FEB-2000 (first entry)

DE PCR primer for DNA encoding cancer associated antigen KOC-2.

XX Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9954738-A1.

XX 28-OCT-1999.

PF 16-MAR-1999; 99WO-US05766.

XX 17-APR-1998; 98US-0061709.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;

XX WPI; 2000-013284/01.

XX Nucleotides representing cancer-associated genes, used to develop

PT products for the diagnosis, monitoring and treatment of cancers

XX

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CC or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or
 CC granulocyte macrophage-colony stimulating factor (GM-CSF).
 XX
 SQ Sequence 1946 BP; 502 A; 528 C; 553 G; 358 T; 5 other;
 Query Match 100.0%; Score 22; DB 21; Length 1946;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCTTGGCGCTGGCGCTCAG 22
 DB 38 TCCTTGGCGCTGGCGCTCAG 59
 RESULT 3
 AAC27338/c
 ID AAC27338 standard; cDNA; 139 BP.
 XX
 AC AAC27338;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 31413.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX Homo sapiens.
 OS
 FN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-500381/45.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 31413; 71pp + CD-ROM; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 SQ Sequence 139 BP; 26 A; 44 C; 54 G; 14 T; 1 other;
 Query Match 80.9%; Score 17.8; DB 21; Length 139;
 Best Local Similarity 90.5%; Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CCTTGGCGCTGGCGCTCAG 22
 DB 50 CCTTGGCGCTGGCGCTCAG 30

PS Claim 108; Page 13; 44pp; English.
 XX PCR primers AAZ36157-58 were used to amplify a cancer associated antigen
 CC gene designated KOC-2. The specification also describes a cancer
 CC associated antigen designated CT7. The CT7 polynucleotide was isolated
 CC from SK-MEL-37 melanoma cells. The polypeptide has some homology with
 CC MAGE-10, limited to about 210 carboxy terminal amino acids. The amino
 CC terminal of the protein has a repetitive pattern, with repeats rich in
 CC serine, proline, glutamine and leucine, and an almost invariable core of
 CC the peptide given in AAY43877. The CT7 polypeptide can be processed to
 CC peptides which provoke lysis by cytolytic T cells. The polynucleotides
 CC and polypeptides can be used for treating a cancerous condition and
 CC screening for or diagnosing cancerous conditions. The cancer associated
 CC antigens can be used as an immunogenic or vaccine composition with an
 CC adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony
 CC stimulating factor (GM-CSF).
 XX
 SQ Sequence 22 BP; 1 A; 9 C; 7 G; 5 T; 0 other;
 Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCTTGGCGCTGGCGCTCAG 22
 DB 1 TCCTTGGCGCTGGCGCTCAG 22
 RESULT 2
 AAZ36153
 ID AAZ36153 standard; DNA; 1946 BP.
 XX
 AC AAZ36153;
 XX
 DT 11-FEB-2000 (first entry)
 XX
 DE An alternative form of DNA encoding cancer associated antigen KOC-2.
 XX
 KW Cancer associated antigen; KOC-2; cancer; vaccine; CT7; ss.
 XX Homo sapiens.
 OS
 FN WO9954738-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 16-MAR-1999; 99WO-US05766.
 XX
 PR 17-APR-1998; 98US-0061709.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Chen Y, Gure A, Taang S, Stockert E, Jager E, Knuth A, Old LJ;
 XX WPI; 2000-013284/01.
 XX
 PT Nucleotides representing cancer-associated genes, used to develop
 PT products for the diagnosis, monitoring and treatment of cancers -
 XX Claim 55; Page 42; 44pp; English.
 XX
 CC The present sequence represents an alternative form of a cancer
 CC associated antigen gene designated KOC-2. The specification also
 CC describes a cancer associated antigen designated CT7. The CT7
 CC polynucleotide has some homology with MAGE-10, limited to about 210 carboxy
 CC terminal amino acids. The amino terminal of the protein has a repetitive
 CC pattern, with repeats rich in serine, proline, glutamine and leucine,
 CC and an almost invariable core of the peptide given in AAY43877. The CT7
 CC polypeptide can be processed to peptides which provoke lysis by
 CC cytolytic T cells. The polynucleotides and polypeptides can be used for
 CC treating a cancerous condition and screening for or diagnosing cancerous
 CC conditions. The cancer associated antigens can be used as an immunogenic

RESULT 4
AAH07034/C
ID AAH07034 standard; cDNA; 711 BP.
XX
AC AAH07034;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:3869.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 1; SEQ ID 3869; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers are also useful for the
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 711 BP; 149 A; 239 C; 209 G; 111 T; 3 other;
Query Match 80.9%; Score 17.8; DB 22; Length 711;
Best Local Similarity 90.5%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CCTTGGCGCTGCGCCCTCAG 22
|||||

Db 39 CCTTGGCGCTGCGCCCTCAG 19
RESULT 5
AAS68110/C
ID AAS68110 standard; cDNA; 1785 BP.
XX
AC AAS68110;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #3914.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR P-PSDB; ABG03923.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID NO 3914; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1785 BP; 416 A; 497 C; 517 G; 355 T; 0 other;
Query Match 80.9%; Score 17.8; DB 23; Length 1785;
Best Local Similarity 90.5%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CCTTGGCGCTGCGCCCTCAG 22
|||||

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AAH14706/c
ID AAH14706 standard; CDNA; 2082 BP.
XX
AC AAH14706;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:12421.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
KW Homo sapiens.
OS
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 12421; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC polynucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 2082 BP; 416 A; 684 C; 607 G; 375 T; 0 other;

Query Match 80.9%; Score 17.8; DB 22; Length 2082;
Best Local Similarity 90.5%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CCTTGGCGCTGCGCTCAG 22
DB 39 CCTTGGCGCTGCGCTCAG 19

RESULT 6
AAST73402
ID AAST73402 standard; CDNA; 1785 BP.
XX
AC AAST73402;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #9206.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
KW Homo sapiens.
OS
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PR 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG09215.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 9206; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful for treating
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1785 BP; 355 A; 517 C; 497 G; 416 T; 0 other;

Query Match 80.9%; Score 17.8; DB 23; Length 1785;
Best Local Similarity 90.5%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CCTTGGCGCTGCGCTCAG 22
DB 931 CCTTGGCGCTGCGCTCAG 951

RESULT 7

RESULT 8
AAK63986/c
ID AAK63986 standard; cDNA; 464 BP.
XX AC AAK63986;
XX DT 06-NOV-2001 (first entry)
XX XX Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:9046.
DE Human; Immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ss.
KW Homo sapiens.
XX WO200157182-A2.
PN 09-AUG-2001.
PD 17-JAN-2001; 2001WO-US01354.
PF 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-02331968.
PR 14-SEP-2000; 2000US-0233297.
PR 14-SEP-2000; 2000US-0233298.
PR 14-SEP-2000; 2000US-0233299.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234998.
PR 27-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
DR P-PSDB; AAM91205.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Claim 1; SEQ ID NO 9046; 3071pp + Sequence Listing; English.
PS
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK4703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 464 BP; 131 A; 115 C; 110 G; 107 T; 1 other;
SQ
Query Match 78.2%; Score 17.2; DB 22; Length 464;
Best Local Similarity 86.4%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TCCTTGGCGCTGGCGCTCAG 22
Db 200 TCCTTGGCGCTGGCGCTCTG 179
RESULT 9
ABL29179/c
ID ABL29179 standard; DNA; 1217 BP.
XX
XX ABL29179;
AC
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 39010.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PR (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 39010; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABBS7737-ABBY2072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1217 BP; 301 A; 328 C; 358 G; 230 T; 0 other;
SQ
Query Match 78.2%; Score 17.2; DB 23; Length 1217;
Best Local Similarity 86.4%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TCCTTGGCGCTGGCGCTCAG 22
Db 1066 TCCTTGGCGCTGGCGCTCAG 1045
RESULT 10
ABL29178/c
ID ABL29178 standard; DNA; 3408 BP.
XX
XX ABL29178;
AC
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 39007.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PR (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX

PF 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 39010; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABBS7737-ABBY2072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1217 BP; 301 A; 328 C; 358 G; 230 T; 0 other;
SQ
Query Match 78.2%; Score 17.2; DB 23; Length 1217;
Best Local Similarity 86.4%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TCCTTGGCGCTGGCGCTCAG 22
Db 1066 TCCTTGGCGCTGGCGCTCAG 1045
RESULT 10
ABL29178/c
ID ABL29178 standard; DNA; 3408 BP.
XX
XX ABL29178;
AC
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 39007.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PR (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX

XX PS Claim 1; SEQ ID NO 39007; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511); expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 3408 BP; 945 A; 779 C; 790 G; 894 T; 0 other;
 Query Match 78.2%; Score 17.2; DB 23; Length 3408;
 Best Local Similarity 86.4%; Pred. No. 2.6e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TCCTTGGCGCTGCGGCTCAG 22
 ||||| ||||| ||||| |||||
 Db 2257 TCCTTGGCGCTGCGGCTCAG 2236
 RESULT 11
 AAS47110/C
 ID AAS47110 standard; cDNA; 462 BP.
 XX AC AAS47110;
 XX DT 18-DEC-2001 (first entry)
 XX DE Human breast cancer cDNA clone 14382.
 XX KW Human; ss; breast cancer protein; tumour; cancer; cytostatic;
 XX KW gene therapy.
 XX OS Homo sapiens.
 XX PN WO200179286-A2.
 XX PD 25-OCT-2001.
 XX PF 12-APR-2001; 2001WO-US12164.
 XX PR 17-APR-2000; 2000US-0551621.
 PR 08-JUN-2000; 2000US-0590751.
 PR 22-JUN-2000; 2000US-0604287.
 PR 20-JUL-2000; 2000US-0620405.
 XX PA (CORI-) CORIXA CORP.
 XX PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
 XX DR WPI; 2001-611721/70.
 XX PT Breast Tumour Proteins and nucleic acids useful for the prevention,
 PT diagnosis and treatment of breast cancer -
 XX Claim 37; Page 193; 297pp; English.
 XX CC The invention relates to isolated breast tumour proteins and
 CC nucleic acids that encode them, including immunogenic fragments of the
 CC proteins. Also included are expression vectors expressing the
 CC proteins, transformed cells and antibodies raised against the proteins or
 CC an antigen presenting cell expressing the protein. The proteins and
 CC nucleic acids may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate breast tumour protein expression,
 CC i.e. breast tumours and breast cancer e.g. by gene therapy. The nucleic
 CC acids and their complements may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in

CC samples, and therefore which patients may be in need of restorative
 CC therapy. The proteins, nucleic acids and antibodies may be used in assays
 CC to identify modulators (e.g. antagonists) of breast tumour protein
 CC expression and activity. The antibodies and antagonists may also be used
 CC to down regulate expression and activity. The antibodies may also be used
 CC as diagnostic agents for detecting the presence of the proteins in
 CC samples (e.g. by enzyme linked immunosorbent assay (ELISA)) and in other
 CC immuno-purification diagnostic techniques. The present sequence is
 CC a cDNA from a breast tumour cDNA library isolated by subtractive
 CC hybridisation against a normal breast cDNA library.
 XX SQ Sequence 462 BP; 124 A; 108 C; 118 G; 99 T; 13 other;
 Query Match 76.4%; Score 16.8; DB 22; Length 462;
 Best Local Similarity 90.0%; Pred. No. 4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TCCTTGGCGCTGCGGCTC 20
 ||||| ||||| ||||| |||||
 Db 91 TCTTGTCTCGCTGCGGCTC 72
 RESULT 12
 AAF17680/C
 ID AAF17680 standard; cDNA; 462 BP.
 XX AC AAF17680;
 XX DT 13-MAR-2001 (first entry)
 XX DE Human breast cancer associated 14382 coding sequence.
 XX KW Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.
 XX OS Homo sapiens.
 XX PN WO200060076-A2.
 XX PD 12-OCT-2000.
 XX PF 15-FEB-2000; 2000WO-US05308.
 XX PR 02-APR-1999; 99US-0285480.
 PR 23-JUN-1999; 99US-0339338.
 PR 02-SEP-1999; 99US-0389681.
 PR 03-NOV-1999; 99US-0433826.
 XX PA (CORI-) CORIXA CORP.
 XX PI Yuqiu J, Dillon DC, Mitcham JL, Xu J, Harlocker SL;
 XX DR WPI; 2001-122627/13.
 XX PT An isolated polypeptide useful for the treatment and diagnosis of
 PT tumours e.g. breast cancer comprises at least an immunogenic portion of
 PT a breast tumor protein -
 XX Claim 66; Page 138; 238pp; English.
 XX CC The present invention provides the coding sequences and some protein
 CC sequences of proteins associated with breast cancer in humans. These
 CC sequences can be used in the diagnosis and treatment of cancers,
 CC particularly breast tumours.
 XX SQ Sequence 462 BP; 124 A; 108 C; 118 G; 99 T; 13 other;
 Query Match 76.4%; Score 16.8; DB 22; Length 462;
 Best Local Similarity 90.0%; Pred. No. 4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TCCTTGGCGCTGCGGCTC 20
 ||||| ||||| ||||| |||||
 Db 91 TCTTGTCTCGCTGCGGCTC 72

Mon Apr 21 10:29:56 2003

us-09-270-437d-11.rng

```

RESULT 13
AAK95145/c
ID ABK95145 standard; cDNA; 462 BP.
XX
XX
AC ABK95145;
XX
XX
DT 24-SEP-2002 (first entry)
XX
XX
DE Human breast tumour cDNA 14382.
XX
XX
KW Human; ss; breast cancer; cytostatic; gene therapy; SYN22A12; SYN22A2;
KW B723P; B726P.
XX
XX
OS Homo sapiens.
XX
XX
PN US6387697-B1.
XX
XX
PD 14-MAY-2002.
XX
XX
PF 28-DEC-1998; 98US-0222575.
XX
XX
PR 28-DEC-1998; 98US-0222575.
XX
XX
PA (CORI-) CORIXA CORP.
XX
XX
PI Yuqiu J, Dillon DC, Mitcham JL, Xu J;
XX
XX
DR WPI; 2002-478446/51.
XX
XX
PT New nucleic acids encoding breast cancer antigens SYN22A12, SYN22A2, of
PT B723P and B726P, useful for the prevention, diagnosis and treatment of
PT breast cancer.
XX
XX
PS Example 2; Column 147-148; 82pp; English.
XX
XX
CC The invention relates to isolated polynucleotides: (I)-(IV) encoding
CC breast cancer antigens SYN22A12, SYN22A2, B723P and B726P (4 of 172 cDNA
CC sequences included in the specification). Also included are isolated
CC cDNAs comprising sequences with 90 % identity to (I)-(IV), an expression
CC vector comprising the cDNAs, a host cell transformed with the expression
CC vector and a diagnostic kit comprising 2 oligonucleotide primers or
CC probes, where 1 of the oligonucleotide primers or probes is specific
CC for (I)-(IV) and isolated cDNAs comprising sequences with 90 %
CC identity to (I)-(IV), and that is 10 nucleotides in length.
CC These polynucleotide sequences (I) to (IV) and the SYN22A12, SYN22A2,
CC B723P and B726P peptides they encode can be used as diagnostic
CC markers, as models for the development of human therapeutic targets,
CC aid in the identification of therapeutic proteins, and serve as targets
CC for the development of human therapeutic agents that may be used for
CC the treatment of breast cancer. In particular, they may be transfected
CC (using a vector) into a host cell that may be cultured to express the
CC breast cancer antigens. These antigens may then be used in the production
CC of antibodies against SYN22A12, SYN22A2, B723P and B726P, which in turn
CC may be used as immunoassay reagent and therapeutics for the diagnosis and
CC treatment of breast cancer. Short 10 nucleotide sequences of (I) to (IV)
CC may be used as primers and probes in hybridisation and amplification
CC reactions for the detection of SYN22A12, SYN22A2, B723P and B726P in the
CC diagnosis of breast cancer. The present sequence is a breast cancer
CC specific cDNA of the invention.
XX
XX
SQ Sequence 462 BP; 124 A; 108 C; 118 G; 99 T; 13 other;

Query Match 76.4%; Score 16.8; DB 24; Length 462;
Best Local Similarity 90.0%; Pred. No. 4e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2;

Qy 1 TCCTTGGCGCTGGCGCTC 20
Db 91 TCTTTGCTGGCTGGCGCTC 72

RESULT 14
AAK20553/c
ID AAX20553 standard; DNA; 10461 BP.
XX
XX
AC AAX20553;
XX
XX
DT 05-MAY-1999 (first entry)
XX
XX
DE Polynucleotide sequence from the genome of Treponema pallidum.
XX
XX
KW Treponema pallidum infection; syphilis; Borrelia infection; animal;
KW enzyme production; ds.
XX
XX
OS Treponema pallidum.
XX
XX
PN WO9859034-A2.
XX
XX
PD 30-DEC-1998.
XX
XX
PF 23-JUN-1998; 98WO-US13041.
XX
XX
PR 24-JUN-1997; 97US-0050667.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Fraser CW;
XX
XX
DR WPI; 1999-081273/07.
XX
XX
PT New isolated Treponema pallidum nucleic acids - used to develop
PT products for the detection, diagnosis, characterisation, prevention
PT and therapy of T. pallidum infections, particularly syphilis
XX
XX
PS Claim 1; Page 491-497; 1150pp; English.
XX
XX
CC AAX20500-21243 represent polynucleotide sequences from the genome of
CC Treponema pallidum. The sequences can be used for detection,
CC diagnosis, characterisation, prevention and therapy for T. pallidum
CC infections, particularly syphilis. They can also be used for detecting
CC diseases related to Borrelia infections in animals, and for the
CC production of biosynthetic products such as enzymes.
XX
XX
SQ Sequence 10461 BP; 2325 A; 3411 C; 2493 G; 2213 T; 19 other;

Query Match 76.4%; Score 16.8; DB 20; Length 10461;
Best Local Similarity 90.0%; Pred. No. 3.9e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2;

Qy 3 CTTGGCGCTGGCGCTCAG 22
Db 6012 CTTGGCGCTGGCGCTCAG 5993

RESULT 15
AAK98531
ID AAK98531 standard; DNA; 13308 BP.
XX
XX
AC AAK98531;
XX
XX
DT 16-APR-2002 (first entry)
XX
XX
DE Human enolase 3 (beta, muscle) isogene.
XX
XX
KW Human; enolase 3 (beta, muscle); ENO3; single nucleotide polymorphism;
KW SNP; haplotype analysis; isogene; gene; ds.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 4092..9309
FT /tag= a
FT /product= "ENO3"
FT /note= "this sequence contains introns"

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FT allele replace(3640,C)
FT exon /*tag= b
FT exon 4092..4176
FT intron /*tag= c
FT intron /number= "1"
FT intron 4177..5056
FT intron /*tag= d
FT intron /number= "1"
FT intron replace(5039,C)
FT intron /*tag= e
FT intron 5057..5152
FT intron /*tag= f
FT intron /number= "2"
FT intron 5153..5312
FT intron /*tag= g
FT intron /number= "2"
FT intron 5313..5370
FT intron /*tag= h
FT intron /number= "3"
FT intron replace(5343,G)
FT intron /*tag= i
FT intron replace(5357,C)
FT intron /*tag= j
FT intron replace(5366,C)
FT intron /*tag= k
FT intron 5371..5532
FT intron /*tag= l
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FT intron 5533..5603
FT intron /*tag= m
FT intron /number= "4"
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FT intron /*tag= n
FT intron replace(5547,C)
FT intron /*tag= o
FT intron 5604..5973
FT intron /*tag= p
FT intron /number= "4"
FT intron 5974..6107
FT intron /*tag= q
FT intron /number= "5"
FT intron 6108..7336
FT intron /*tag= r
FT intron /number= "5"
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FT intron /*tag= t
FT intron /number= "6"
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FT intron /*tag= u
FT intron /number= "6"
FT intron 7669..7866
FT intron /*tag= v
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FT intron /*tag= w
FT intron 7867..8203
FT intron /*tag= x
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FT intron /*tag= y
FT intron 8204..8405
FT intron /*tag= z
FT intron /number= "8"
FT intron replace(8332,G)
FT intron /*tag= aa
FT intron 8406..8834
FT intron /*tag= ab
FT intron /number= "8"
FT intron replace(8423,C)
FT intron /*tag= ac
FT intron 8835..8943

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FT intron /*tag= ad
FT intron /number= "9"
FT intron 8944..9092
FT intron /*tag= ae
FT intron /number= "9"
FT intron replace(8951,C)
FT intron /*tag= af
FT intron 9093..9151
FT intron /*tag= ag
FT intron /number= "10"
FT intron 9152..9239
FT intron /*tag= ah
FT intron /number= "10"
FT intron replace(9154,G)
FT intron /*tag= ai
FT intron 9240..9309
FT intron /*tag= aj
FT intron /number= "11"
FT intron replace(9431,G)
FT intron /*tag= ak

```

WO200202579-A2.

10-JAN-2002.

02-JUL-2001; 2001WO-US20952.

30-JUN-2000; 2000US-215236P.

(GENA-) GENAISSANCE PHARM INC.

Duda A, Finkel K, Koshy B, Parks KE;

WPI; 2002-154721/20.

P-PSDB; AAM48922.

Novel genetic variants of enolase 3, (beta, muscle) gene useful in studying expression and function of the protein, and for screening drugs to treat disorders of glycolytic pathway -

Claim 20; Fig 1; 90pp; English.

The present invention provides the protein, cDNA and genomic sequences of a human enolase 3 (beta, muscle) isoenzyme containing a number of single nucleotide polymorphisms (SNPs). The sequences can be used to identify the haplotype of an individual and identify whether particular haplotypes are linked to certain diseases. The present sequence is the ENO3 gene.

Sequence 13308 BP; 2874 A; 3775 C; 3758 G; 2901 T; 0 other;

Query Match 76.4%; Score 16.8; DB 24; Length 13308;

Best Local Similarity 90.0%; Pred. No. 3.9e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTTGGCGCTGCGCTCA 21

Db 1405 CCGTGGCGCTGCGCTCA 1424

Search completed: April 18, 2003, 05:45:23

Job time : 103 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	22	100.0	1946	4	US-09-061-709-7	Sequence 7, Appli	
2	17.2	78.2	1704	4	US-09-608-917A-3	Sequence 3, Appli	
C 3	16.8	76.4	462	4	US-09-222-575-165	Sequence 165, App	
4	16.2	73.6	2409	4	US-09-230-225B-3	Sequence 3, Appli	
C 5	15.8	71.8	1471	4	US-09-492-985-11	Sequence 11, Appl	
C 6	15.8	71.8	3744	2	US-08-348-353-16	Sequence 16, Appl	
C 7	15.8	71.8	3744	2	US-08-465-955-16	Sequence 16, Appl	
C 8	15.8	71.8	3744	3	US-08-465-956-16	Sequence 16, Appl	
C 9	15.6	70.9	783	3	US-08-264-861A-11	Sequence 11, Appl	
C 10	15.6	70.9	783	5	PCF-US95-07784-11	Sequence 11, Appl	
C 11	15.6	70.9	1150	1	US-08-264-861A-10	Sequence 10, Appl	
C 12	15.6	70.9	1150	5	PCF-US95-07784-10	Sequence 10, Appl	
13	15.4	70.0	1263	2	US-08-828-488-6	Sequence 6, Appli	
14	15.4	70.0	1363	4	US-09-298-689A-6	Sequence 6, Appli	
C 15	15.4	70.0	2936	2	US-08-738-172-1	Sequence 1, Appli	
C 16	15.2	69.1	423	1	US-08-470-179-127	Sequence 127, App	
17	15.2	69.1	1588	1	US-08-706-037-24	Sequence 24, Appl	
18	15.2	69.1	1588	2	US-09-005-397-24	Sequence 24, Appl	
19	15.2	69.1	1672	1	US-08-172-331B-13	Sequence 13, Appl	
20	15.2	69.1	1943	4	US-09-282-305-7	Sequence 7, Appli	
21	15.2	69.1	3175	1	US-08-050-684-1	Sequence 1, Appli	
C 22	15.2	69.1	3175	1	US-08-582-719-1	Sequence 1, Appli	
C 23	15.2	69.1	5919	4	US-09-221-017B-584	Sequence 584, App	
C 24	15.2	69.1	80161	3	US-09-036-987A-1	Sequence 1, Appli	
C 25	15.2	69.1	80161	4	US-09-370-700-1	Sequence 1, Appli	
C 26	14.8	67.3	391	3	US-08-516-859A-104	Sequence 104, App	
C 27	14.8	67.3	391	4	US-09-586-472-104	Sequence 104, App	

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; LOCATION: (437)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-222-575-165

Query Match          76.4%; Score 16.8; DB 4; Length 462;
Best Local Similarity 90.0%; Pred.No.67;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  TCCTTGGCGGCTGCGGCCTC 20
Db       1  TCTTTGCTGCTGCGGCCTC 72

RESULT 4
US-09-230-225B-3
; Sequence 3, Application US/09230225B
; Patent No. 6403362
; GENERAL INFORMATION:
; APPLICANT: Meiji Seika Kaisha, Ltd.
; APPLICANT: Moriya, Tatsuki
; TITLE OF INVENTION: Systems for the Mass Production of Proteins or Peptides
; TITLE OF INVENTION: of the Genus Humicola
; FILE REFERENCE: VX90054
; CURRENT APPLICATION NUMBER: US/09/230,225B
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 2409
; TYPE: DNA
; ORGANISM: Humicola insolens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (389)..(457)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (458)..()
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (458)..(477)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (478)..(535)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (536)..(1029)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (1030)..(1141)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (1142)..(1761)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (1762)..(1815)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (1816)..(1989)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (1990)..(2044)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (2045)..(2095)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (688)..(693)
; OTHER INFORMATION: Cleavage site SmaI
; NAME/KEY: misc feature
; LOCATION: (1253)..(1259)
; OTHER INFORMATION: Cleavage site BamHI

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NAME/KEY: misc feature
 LOCATION: (1505)..(1510)
 OTHER INFORMATION: Cleavage site BgIII
 NAME/KEY: misc feature
 LOCATION: (1643)..(1648)
 OTHER INFORMATION: Cleavage siteStuI
 US-09-230-225B-3

Query Match
 Best Local Similarity 73.6%; Score 16.2; DB 4; Length 2409;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCTTGGCGCTCGGCGCTCAG 22
 Db 886 CCTTGGCGCTCGGCGCTCGG 906

RESULT 5
 US-09-492-985-11/c
 Sequence 11 Application US/09492985
 Patent No. 6376240
 GENERAL INFORMATION:
 APPLICANT: Song, An M.
 APPLICANT: Chen, Ya-Pen
 APPLICANT: Krensky, Alan M.
 TITLE OF INVENTION: RFLAT-1: A Transcription Factor That
 TITLE OF INVENTION: Activates RANTES Gene Expression
 FILE REFERENCES: SUN-113P
 CURRENT APPLICATION NUMBER: US/09/492,985
 CURRENT FILING DATE: 2000-01-27
 EARLIER APPLICATION NUMBER: 60/117,576
 EARLIER FILING DATE: 1999-01-27
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 1471
 TYPE: DNA
 ORGANISM: mouse
 US-09-492-985-11

Query Match
 Best Local Similarity 71.8%; Score 15.8; DB 4; Length 1471;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTTGGCGCTCGGCGCTC 20
 Db 650 CCTTGGCGCGAGCGGCC 632

RESULT 6
 US-08-348-353-16/c
 Sequence 16, Application US/08348353
 Patent No. 5932217
 GENERAL INFORMATION:
 APPLICANT: Tuomanen, Elaine
 APPLICANT: Masure, Robert
 TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
 TITLE OF INVENTION: Ligand for Leukocyte CR3
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/348,353

FILING DATE: 30-NOV-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson, David
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-097CIP1
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3744 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3744
 PUBLICATION INFORMATION:
 AUTHORS: Delisse-Gathoye, et al.
 TITLE: Cloning, Partial Sequence, Expressions, and
 TITLE: Antigenic Analysis of the Filamentous
 TITLE: Hemagglutinin Gene of Bordetella Pertussis
 JOURNAL: Infection and Immunity
 VOLUME: 58
 ISSUE: 9
 PAGES: 2895-2905
 DATE: September-1990
 US-08-348-353-16

Query Match
 Best Local Similarity 71.8%; Score 15.8; DB 2; Length 3744;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCTTGGCGCTCGGCGCT 19
 Db 3050 TCCTTGGCGCTCGGCGAT 3032

RESULT 7
 US-08-465-965-16/c
 Sequence 16, Application US/08465965
 Patent No. 5968512
 GENERAL INFORMATION:
 APPLICANT: Tuomanen, Elaine
 APPLICANT: Masure, Robert
 TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
 TITLE OF INVENTION: Ligand for Leukocyte CR3
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,965
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/348,353
 FILING DATE: 30-NOV-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/247,572
 FILING DATE: 23-MAY-1994
 CLASSIFICATION: 424

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIP1DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3744
PUBLICATION INFORMATION:
AUTHORS: Delisse-Gathoye, et al.
TITLE: Cloning, Partial Sequence, Expressions, and
TITLE: Antigenic Analysis of the Filamentous
TITLE: Hemagglutinin Gene of Bordetella Pertussis
JOURNAL: Infection and Immunity
VOLUME: 58
ISSUE: 9
PAGES: 2895-2905
DATE: September-1990
US-08-465-965-16

Query Match 71.8%; Score 15.8; DB 2; Length 3744;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCTTGGCGCTCGGCCT 19
DB 3050 TCCTTGGCGCTCGGCAT 3032

RESULT 8
US-08-465-966-16/C
Sequence 16, Application US/08465966
Patent No. 6015560
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,966
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353

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FILING DATE: 30-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIP1DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3744
PUBLICATION INFORMATION:
AUTHORS: Delisse-Gathoye, et al.
TITLE: Cloning, Partial Sequence, Expressions, and
TITLE: Antigenic Analysis of the Filamentous
TITLE: Hemagglutinin Gene of Bordetella Pertussis
JOURNAL: Infection and Immunity
VOLUME: 58
ISSUE: 9
PAGES: 2895-2905
DATE: September-1990
US-08-465-966-16

Query Match 71.8%; Score 15.8; DB 3; Length 3744;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCTTGGCGCTCGGCCT 19
DB 3050 TCCTTGGCGCTCGGCAT 3032

RESULT 9
US-08-264-861A-11/c
Sequence 11, Application US/08264861A
Patent No. 5622866
GENERAL INFORMATION:
APPLICANT: MOTAMED, HAIDEB
APPLICANT: SHAFIEE, ALI
TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. ERIC THIES
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,861A
; FILING DATE: 23-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: THIES, J. ERIC
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-264-861A-11

Query Match 70.9%; Score 15.6; DB 1; Length 783;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGCTCAG 22
Db 401 TCCTTGGCGGCGCGGCTCG 380

RESULT 11
US-08-264-861A-10/c
; Sequence 10, Application US/08264861A
; Patent No. 5622866
; GENERAL INFORMATION:
; APPLICANT: MOTAMEDI, HAIDEH
; APPLICANT: SHAFIEE, ALI
; TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
; TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
; TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. ERIC THIES
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,861A
; FILING DATE: 23-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: THIES, J. ERIC
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-264-861A-10

Query Match 70.9%; Score 15.6; DB 1; Length 1150;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGCTCAG 22
Db 462 TCCTTGGCGGCGCGGCTCG 441

RESULT 12
PCT-US95-07784-10/c
; Sequence 10, Application PC/TUS9507784
; GENERAL INFORMATION:
; APPLICANT: MOTAMEDI, HAIDEH
; APPLICANT: SHAFIEE, ALI
; TITLE OF INVENTION: EXPRESSION CASSETTES USEFUL IN
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us-09-270-437d-11.rni

Mon Apr 21 10:29:58 2003

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; TITLE OF INVENTION: CONSTRUCTION OF INTEGRATIVE AND REPLICATIVE EXPRESSION
; TITLE OF INVENTION: VECTORS FOR STREPTOMYCES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. ERIC THIES
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07784
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: THIES, J. ERIC
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3904
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US95-07784-10

Query Match 70.9%; Score 15.6; DB 5; Length 1150;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCTTGGCGGCTGGGCTCAG 22
Db 462 TCCTTGGCGGCGGCGGCTCG 441

RESULT 13
US-08-828-488-6
; Sequence 6, Application US/08828488
; Patent No. 5925521
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,488
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,488
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0241 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1263 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNCR01
; CLONE: 770469
; US-08-828-488-6

Query Match 70.0%; Score 15.4; DB 2; Length 1263;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCTTGGCGGCTGGCGC 17
Db 19 TCCTTGGCGGCGCGGC 35

RESULT 14
US-09-299-689A-6
; Sequence 6, Application US/09299689A
; Patent No. 6379913
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN SERINE
; TITLE OF INVENTION: CARBOXYPEPTIDASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,689A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,488
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0241 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1263 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNCR101
CLONE: 770469
US-09-299-689A-6

Query Match 70.0%; Score 15.4; DB 4; Length 1263;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCTTGGCGGCTGCGGC 17
Db 19 TCCTTGGCGGCGCGGC 35

RESULT 15

US-08-738-172-1
; Sequence 1, Application US/08738172
; Patent No. 5939257
; GENERAL INFORMATION:
; APPLICANT: Szasz, Joseph
; APPLICANT: Davis, Maria
; TITLE OF INVENTION: THERMOSTABLE ALKALINE PHOSPHATASES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,172
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,965
; FILING DATE: October 27, 1995
; APPLICATION NUMBER: 08/465,003
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/575,354
; FILING DATE: December 20, 1995
; APPLICATION NUMBER: 08/240,158
; FILING DATE: May 10, 1994
; APPLICATION NUMBER: 08/229,329
; FILING DATE: April 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 222/158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2936 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-738-172-1

Query Match 70.0%; Score 15.4; DB 2; Length 2936;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCTTGGCGGCTGCGGC 17
Db 1111 TCCTTGGCGGCTGCGGC 1127

Search completed: April 18, 2003, 07:34:29
Job time : 27.5 secs

GenCore version 5.1.4_P5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:31 ; Search time 91.3333 Seconds
(without alignments)
241.975 Million cell updates/sec

Title: US-09-270-437D-11

Perfect score: 22

Sequence: 1 TCCTTGGCGCTGGCGCTCAG 22

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IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 1279498

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	16.8	76.4	386	10	US-09-960-352-11656
3	16.8	76.4	462	9	US-10-076-622-165
4	16.8	76.4	462	10	US-09-604-287A-165
5	16.8	76.4	462	10	US-09-339-338-165
6	16.8	76.4	462	12	US-10-007-805-165
7	16.4	74.5	1641	10	US-09-808-387-27
8	16.4	74.5	1759	9	US-09-992-598-180
9	16.4	74.5	1759	9	US-09-989-293A-180
10	16.4	74.5	1759	9	US-09-989-735-180
11	16.4	74.5	1759	9	US-09-990-444-180
12	16.4	74.5	1759	9	US-09-989-730-180
13	16.4	74.5	1759	9	US-09-930-436-180
14	16.4	74.5	1759	9	US-09-981-181-180
15	16.4	74.5	1759	9	US-09-993-687-180
16	16.4	74.5	1759	9	US-09-989-734-180
17	16.4	74.5	1759	9	US-09-997-653-180
18	16.4	74.5	1759	9	US-10-174-590-151
19	16.4	74.5	1759	9	US-10-176-758-151

20	16.4	74.5	1759	9	US-10-175-737-151	Sequence 151, App
21	16.4	74.5	1759	9	US-09-993-667-180	Sequence 180, App
22	16.4	74.5	1759	9	US-10-173-706-151	Sequence 151, App
23	16.4	74.5	1759	9	US-10-175-738-151	Sequence 151, App
24	16.4	74.5	1759	9	US-10-175-752-151	Sequence 151, App
25	16.4	74.5	1759	9	US-10-176-482-151	Sequence 151, App
26	16.4	74.5	1759	9	US-10-176-757-151	Sequence 151, App
27	16.4	74.5	1759	9	US-10-176-913-151	Sequence 151, App
28	16.4	74.5	1759	9	US-10-180-552-151	Sequence 151, App
29	16.4	74.5	1759	9	US-10-180-557-151	Sequence 151, App
30	16.4	74.5	1759	9	US-09-990-438-180	Sequence 180, App
31	16.4	74.5	1759	9	US-09-990-562-180	Sequence 180, App
32	16.4	74.5	1759	9	US-09-997-428-180	Sequence 180, App
33	16.4	74.5	1759	9	US-09-997-666-180	Sequence 180, App
34	16.4	74.5	1759	9	US-10-173-700-151	Sequence 151, App
35	16.4	74.5	1759	9	US-10-174-572-151	Sequence 151, App
36	16.4	74.5	1759	9	US-10-174-579-151	Sequence 151, App
37	16.4	74.5	1759	9	US-10-174-582-151	Sequence 151, App
38	16.4	74.5	1759	9	US-10-174-588-151	Sequence 151, App
39	16.4	74.5	1759	9	US-10-175-739-151	Sequence 151, App
40	16.4	74.5	1759	9	US-10-175-740-151	Sequence 151, App
41	16.4	74.5	1759	9	US-10-175-743-151	Sequence 151, App
42	16.4	74.5	1759	9	US-10-176-488-151	Sequence 151, App
43	16.4	74.5	1759	9	US-10-176-492-151	Sequence 151, App
44	16.4	74.5	1759	9	US-10-176-747-151	Sequence 151, App
45	16.4	74.5	1759	9	US-10-176-750-151	Sequence 151, App

ALIGNMENTS

RESULT 1

US-09-899-651-7
; Sequence 7, Application US/09899651
; Patent No. US2002011470A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Yao-Tseng

; APPLICANT: Teang, Solam

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Jager, Elke

; APPLICANT: Knuth, Alexander

; APPLICANT: Old, Lloyd J.

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated

; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof

; FILE REFERENCE: LUD 538

; CURRENT APPLICATION NUMBER: US/09/899,651

; PRIOR FILING DATE: 2001-07-06

; PRIOR APPLICATION NUMBER: US/09/061,709

; PRIOR FILING DATE: 1998-04-17

; NUMBER OF SEQ ID NOS: 8

; SEQ ID NO 7

; LENGTH: 1946

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

US-09-899-651-7

Query Match

Best Local Similarity 100.0%; Score 22; DB 10; Length 1946;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTTGGCGCTGGCGCTCAG 22

Db 38 TCCTTGGCGCTGGCGCTCAG 59

RESULT 2

US-09-960-352-11656/c

; Sequence 11656, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

us-09-270-437d-11.rnpb

Mon Apr 21 10:30:00 2003

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; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11656
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 50-LIB3057-003-Q1-K1-E10
US-09-960-352-11656

Query Match          76.4%; Score 16.8; DB 10; Length 386;
Best Local Similarity 90.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGGCTGCGGCCTCA 21
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Db 326 CCTTGGCGGCTGCGGCCTCA 307

RESULT 3
US-10-076-622-165/c
; Sequence 165, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10, 33, 36, 49, 198, 223, 243, 278, 357, 385, 399, 405, 437
; OTHER INFORMATION: n = A,T,C or G
US-10-076-622-165

Query Match          76.4%; Score 16.8; DB 9; Length 462;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGCGGCCTC 20
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Db 91 TCCTTGGCTGCTGCGGCCTC 72

RESULT 4
US-09-604-287A-165/c
; Sequence 165, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

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; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(462)
; OTHER INFORMATION: n = A,T,C or G
US-09-604-287A-165

Query Match          76.4%; Score 16.8; DB 10; Length 462;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGCGGCCTC 20
    ||||| ||||| ||||| |||||
Db 91 TCCTTGGCTGCTGCGGCCTC 72

RESULT 5
US-09-339-338-165/c
; Sequence 165, Application US/09339338A
; Patent No. US20020102602A1
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(462)
; OTHER INFORMATION: n = A,T,C or G
US-09-339-338-165

Query Match          76.4%; Score 16.8; DB 10; Length 462;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGCGGCCTC 20
    ||||| ||||| ||||| |||||
Db 91 TCCTTGGCTGCTGCGGCCTC 72

RESULT 6
US-10-007-805-165/c
; Sequence 165, Application US/10007805
; Patent No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.

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; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10, 33, 36, 49, 198, 222, 243, 278, 357, 385, 399, 405, 437
; OTHER INFORMATION: n = A,T,C or G
US-10-007-805-165

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Query Match          76.4%; Score 16.8; DB 12; Length 462;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 TCCTGGCGGCTGGCGCTC 20
Db 91 TCCTGGCTGGCGGCTC 72

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RESULT 7
US-09-808-387-27
; Sequence 27, Application US/09808387
; Patent No. US20020132293A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; APPLICANT: Tonis Timmusk
; APPLICANT: Celmines Research
; TITLE OF INVENTION: MAMMALIAN NEUTRALIZED FAMILY OF
; FILE REFERENCE: TRANSCRIPTION REGULATORS AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/09/808,387
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1641
; TYPE: DNA
; ORGANISM: Rat
US-09-808-387-27

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Query Match          74.5%; Score 15.4; DB 10; Length 1641;
Best Local Similarity 94.4%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 TCCTTGGCGGCTGGCGGCC 18
Db 1011 TCCTGGCGGCTGGCGGCC 1028

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RESULT 8
US-09-992-598-180
; Sequence 180, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

```

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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
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; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088167
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; PRIOR APPLICATION NUMBER: 60/088202
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09

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Mon Apr 21 10:30:00 2003

;; PRIOR APPLICATION NUMBER: 60/088734
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742
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;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
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;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
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;; PRIOR FILING DATE: 1998-06-23
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;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535

Query Match 74.5%; Score 16.4; DB 9; Length 1759;
Best Local Similarity 94.4%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 TCGCGCTGCTGCTCAG 22
Db 98 TCGCGCTGCTGCTCAG 115
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RESULT 9
US-09-989-293A-180
; Sequence 180, Application US/09989293A
; Patent No. US2002017164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-07-09

Query Match          74.5%; Score 16.4; DB 9; Length 1759;
Best Local Similarity 94.4%; Pred No. 73;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TGCGCGCTGCGGCTCAG 22
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DB 98 TGCGCGCTGCTGCTCAG 115

RESULT 10
US-09-989-735-180
; Sequence 180, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 74.5%; Score 16.4; DB 9; Length 1759;
 Best Local Similarity 94.4%; Pred. No. 73;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TCGCGCTGCGGCTCAG 22
 Dd 98 TCGCGCTGCTGCTCAG 115

RESULT 11
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 ; Sequence 180, Application US/0990444
 ; Publication No. US20020193300A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: E2730PIC19
 ; CURRENT APPLICATION NUMBER: US/09/990,444
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16

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Query Match 74.5%; Score 16.4; DB 9; Length 1759;
Best Local Similarity 94.4%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TCGCGCTGCGGCTCAG 22
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RESULT 12
US-09-989-730-180
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; Publication No US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Iivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC9
; CURRENT APPLICATION NUMBER: US/09/989,730
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 ; PRIOR FILING DATE: 1998-06-24
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 74.5%; Score 16.4; DB 9; Length 1759;
 Best Local Similarity 94.4%; Pred. No. 73;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TCGCGCTCGCGCTCAG 22
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 Db 98 TCGCGCTCGCGCTCAG 115

RESULT 13
 US-09-990-436-180
 ; Sequence 180, Application US/09990436
 ; Publication No. US20020198148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730P1C14
 ; CURRENT APPLICATION NUMBER: US/09/990,436
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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 ; PRIOR APPLICATION NUMBER: 60/065311
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 ; PRIOR APPLICATION NUMBER: 60/066770
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 ; PRIOR APPLICATION NUMBER: 60/075945
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 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
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 ; PRIOR FILING DATE: 1998-04-28

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; PRIOR FILING DATE: 1998-07-09

Query Match          74.5%; Score 16.4; DB 9; Length 1759;
Best Local Similarity 94.4%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Publication No. US20020197615A1
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 74.5%; Score 16.4; DB 9; Length 1759;
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QY 5 TGGCGCGCTGCGGCTCAG 22
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RESULT 15

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 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tuma, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730PIC11
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Query Match	Score 16.4;	DB 9;	Length 1759;
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Qy 5 TCGCGCTGCGGCTCAG 22
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PRIOR APPLICATION NUMBER:	60/089952

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Search completed: April 18, 2003, 10:14:05
Job time : 94.5 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 05:48:17 ; Search time 1211 seconds
(without alignments)
456.759 Million cell updates/sec

Title: US-09-270-437D-11

Perfect score: 22
Sequence: 1 tcttgcgcgtcgcgcctcag 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 67: /cgn2_6/ptodata/1/pna/US6023 COMB.seq.*
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- 69: /cgn2_6/ptodata/1/pna/US6025 COMB.seq.*
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- 79: /cgn2_6/ptodata/1/pna/US6035 COMB.seq.*
- 80: /cgn2_6/ptodata/1/pna/US6036 COMB.seq.*
- 81: /cgn2_6/ptodata/1/pna/US6037 COMB.seq.*
- 82: /cgn2_6/ptodata/1/pna/US6038 COMB.seq.*
- 83: /cgn2_6/ptodata/1/pna/US6039 COMB.seq.*
- 84: /cgn2_6/ptodata/1/pna/US6040 COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	22	100.0	1946	16	US-09-270-437-7
2	22	100.0	1946	33	US-09-899-651-7
3	18.8	85.5	270	20	US-09-535-896-28782
C 4	18.8	85.5	525	18	US-09-417-507-8435
C 5	18	81.8	445	27	US-09-696-864A-7808
C 6	18	81.8	445	60	US-09-161-619-7647
C 7	18	81.8	1166	42	US-10-219-999-7854
C 8	17.8	80.9	214	7	US-08-369-881-2595
C 9	17.8	80.9	214	8	US-08-408-872-939
C 10	17.8	80.9	214	20	US-09-535-896-13145
C 11	17.8	80.9	283	14	US-09-050-817-727
C 12	17.8	80.9	283	16	US-09-270-849B-135409
C 13	17.8	80.9	283	21	US-09-540-2108-7050
C 14	17.8	80.9	283	48	US-09-043-792-727
C 15	17.8	80.9	301	6	US-08-221-623B-3280
C 16	17.8	80.9	301	6	US-08-221-623B-3280
C 17	17.8	80.9	301	6	US-08-221-623B-3280
C 18	17.8	80.9	301	6	US-08-221-623B-3280
C 19	17.8	80.9	301	6	US-08-221-623B-3280
C 20	17.8	80.9	301	6	US-08-221-623B-3280
C 21	17.8	80.9	301	6	US-08-221-623B-3280

Sequence 7, Appli
Sequence 7, Appli
Sequence 28782, A
Sequence 8435, Ap
Sequence 7808, Ap
Sequence 7647, Ap
Sequence 7854, Ap
Sequence 2595, Ap
Sequence 939, Ap
Sequence 13145, A
Sequence 727, App
Sequence 135409,
Sequence 7050, Ap
Sequence 727, App
Sequence 3280, Ap
Sequence 3280, Ap
Sequence 13454, A
Sequence 68226, A
Sequence 68226, A
Sequence 68226, A

ALIGNMENTS

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/ C- LENGTH: 1946
/
/ TYPE: DNA
/
/ ORGANISM: Homo sapiens
/
/ FEATURE:
/
US-09-270-437-7

```

RESULT 2
US-09-899-651-7
; Sequence 7, Application US/09899651
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Teang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.

Query Match	100.0%;	Score 22;	DB 33;	Length 1946;
Best Local Similarity	100.0%;	Pred. No. 38;		
Matches 22:	Conservative 0;	Mismatches 0;	Indels 0	

```

RESULT 3
US-09-535-28782
; Sequence 28782, Application US/09535896
; GENERAL INFORMATION:
; APPLICANT: Sellhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES
; FILE REFERENCE: PD-1003 CIP
; CURRENT APPLICATION NUMBER: US/09/535,896
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 46268
; SOFTWARE: PERL Program
; SEQ ID NO 28782

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```

? TYPE: DNA
? ORGANISM: Homo sapiens
?
? FEATURE:
? NAME: misc feature
? TIME INFORMATION: Incyte ID No: hu00928771
? LOC/KEY: unsure
? LOCATION: 88
?
? OTHER INFORMATION: a, t, c, g, or other
? uc-09-535-896-28782

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Query Match	85.5%;	Score 18.8;	DB 20;	Length 270;
Best Local Similarity	90.9%;	Pred. No. 9.1e+02;		
Matches	20;	Conservative	0; Mismatches	2; Indels
Q1	1	TCCTTGGCGCTGGCGCTCAG	22	
	26	TCCTTTGCGCGCGGCTCAG	47	

RESULT 4
US-09-417-507-8435/c
Sequence 8435, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND DNA
; TITLE OF INVENTION: FUMIGATUS FOR DIA
; FILE REFERENCES: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417
; CURRENT FILING DATE: 1999-10-14

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; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 8435
; LENGTH: 525
; TYPE: DNA
; ORGANISM: A.fumigatus
US-09-417-507-8435

Query Match      85.5%; Score 18.8; DB 18; Length 525;
Best Local Similarity 90.9%; Pred. No. 8.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCTTGGCGCTGCGGCCTCAG 22
   |||||
Db 497 TCCTTGGCACTGCGTCTCAG 476

RESULT 5
US-09-696-664A-7808/c
; Sequence 7808, Application US/09696664A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51721)B
; CURRENT APPLICATION NUMBER: US/09/696,664A
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/161,619
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 17472
; SEQ ID NO 7808
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-048-P1-K1-E7
US-09-696-664A-7808

Query Match      81.8%; Score 18; DB 27; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGCGGCCT 19
   |||||
Db 355 CCTTGGCGCTGCGGCCT 338

RESULT 6
US-60-161-619-7647/c
; Sequence 7647, Application US/60161619
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(51721)A
; CURRENT APPLICATION NUMBER: US/60/161,619
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 7685
; SEQ ID NO 7647
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-048-P1-K1-E7
US-60-161-619-7647

; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 8435
; LENGTH: 525
; TYPE: DNA
; ORGANISM: A.fumigatus
US-09-417-507-8435

Query Match      85.5%; Score 18.8; DB 18; Length 525;
Best Local Similarity 90.9%; Pred. No. 8.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCTTGGCGCTGCGGCCTCAG 22
   |||||
Db 497 TCCTTGGCACTGCGTCTCAG 476

RESULT 5
US-09-696-664A-7808/c
; Sequence 7808, Application US/09696664A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51721)B
; CURRENT APPLICATION NUMBER: US/09/696,664A
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/161,619
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 17472
; SEQ ID NO 7808
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-048-P1-K1-E7
US-09-696-664A-7808

Query Match      81.8%; Score 18; DB 27; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGCGGCCT 19
   |||||
Db 355 CCTTGGCGCTGCGGCCT 338

RESULT 6
US-60-161-619-7647/c
; Sequence 7647, Application US/60161619
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(51721)A
; CURRENT APPLICATION NUMBER: US/60/161,619
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 7685
; SEQ ID NO 7647
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-048-P1-K1-E7
US-60-161-619-7647
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Query Match      81.8%; Score 18; DB 60; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGCGGCCT 19
   |||||
Db 355 CCTTGGCGCTGCGGCCT 338

RESULT 7
US-10-219-999-7854/c
; Sequence 7854, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)C
; CURRENT APPLICATION NUMBER: US/10/219,999
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 7854
; LENGTH: 1166
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(832)
; OTHER INFORMATION:
US-10-219-999-7854

Query Match      81.8%; Score 18; DB 42; Length 1166;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGCGGCCT 19
   |||||
Db 404 CCTTGGCGCTGCGGCCT 387

RESULT 8
US-08-369-881-2595/c
; Sequence 2595, Application US/08369881
; GENERAL INFORMATION:
; APPLICANT: Wilde, Craig G.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Bills, Pamela Kay
; APPLICANT: Pham, Mino Thu;
; TITLE OF INVENTION: HUMAN CARDIAC CELL-DERIVED POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 3690
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3330 Hillview Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.0/6.1/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,881
; FILING DATE: Herewith
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US-08-408-872-939

Query Match 80.9%; Score 17.8; DB 8; Length 214;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCTTGCGCGCTGCGGCTCA 21
Db 157 TCCTTGCGCGCTGCGGCTCA 137

RESULT 10

US-09-535-896-13145/c

Sequence 13145, Application US/09535896

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Deleane, Angelo M.

APPLICANT: Stuart, Susan G.

APPLICANT: Stuve, Laura L.

APPLICANT: Mullahy, Sara J.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES

FILE REFERENCE: PD-1003 CIP

CURRENT APPLICATION NUMBER: US/09/535,896

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 46268

SOFTWARE: PERL Program

SEQ ID NO 13145

LENGTH: 214

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No: hu00824962

NAME/KEY: unsure

LOCATION: 16, 59, 104, 106, 126, 170, 194, 196, 200

OTHER INFORMATION: a, t, c, g, or other

US-09-535-896-13145

Query Match 80.9%; Score 17.8; DB 20; Length 214;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCTTGCGCGCTGCGGCTCA 21
Db 157 TCCTTGCGCGCTGCGGCTCA 137

RESULT 11

US-09-050-817-727/c

Sequence 727, Application US/09050817

GENERAL INFORMATION:

APPLICANT: Gooding, Douglas H.

APPLICANT: Stuve, Laura L.

APPLICANT: Stuart, Susan G.

APPLICANT: Ito, Laura Y.

APPLICANT: Akerblom, Ingrid E.

APPLICANT: Deleane, Angelo M.

APPLICANT: Naughton, Rebecca E.

APPLICANT: Klingler, Tod W.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM HUMAN FETAL KIDNEY

NUMBER OF SEQUENCES: 2115

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM: Floppy disk

US-08-369-881-2595

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Barbara J. Luther

REGISTRATION NUMBER: 33,954

REFERENCE/DOCKET NUMBER: PD0019 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-855-0572

INFORMATION FOR SEQ ID NO: 2595:

SEQUENCE CHARACTERISTICS:

LENGTH: 214 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

IMMEDIATE SOURCE:

CLONE: 187978

Query Match 80.9%; Score 17.8; DB 7; Length 214;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCTTGCGCGCTGCGGCTCA 21
Db 157 TCCTTGCGCGCTGCGGCTCA 137

RESULT 9

US-08-408-872-939/c

Sequence 939, Application US/08408872

GENERAL INFORMATION:

APPLICANT: Wilde, Craig G.

APPLICANT: Deleane, Angelo M.

APPLICANT: Bills, Pamela K.

APPLICANT: Pham, Mino T.

APPLICANT: Altus, Christina M.

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: CARDIAC CELL-DERIVED POLYNUCLEOTIDES AND POLYPEPTIDES

NUMBER OF SEQUENCES: 1954

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3330 HILLVIEW AVENUE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/408,872

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: LUTHER, BARBARA J.

REGISTRATION NUMBER: 33954

REFERENCE/DOCKET NUMBER: PD-0032 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 855-0555

TELEFAX: (415) 852-0195

INFORMATION FOR SEQ ID NO: 939:

SEQUENCE CHARACTERISTICS:

LENGTH: 214 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

IMMEDIATE SOURCE:

CLONE: 187978


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/
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/050,817
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/043,792
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CERRONE, MICHAEL C.
/ REGISTRATION NUMBER: 39,132
/ REFERENCE/DOCKET NUMBER: PD-0355P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 855-0555
/ TELEFAX: (415) 845-4166
/ INFORMATION FOR SEQ ID NO: 727:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 283 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ IMMEDIATE SOURCE:
/ CLONE: 2991071H1
/ US-09-050-817-727

Query Match 80.9%; Score 17.8; DB 14; Length 283;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGGCGCTCAG 22
Db 47 CCTTGGCGCTGCAGCCCG 27

RESULT 12
US-09-270-849B-135409/c
/ Sequence 135409, Application US/09270849B
/ GENERAL INFORMATION:
/ APPLICANT: Swimmer et al.
/ TITLE OF INVENTION: Insect genome survey devices
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/09/270,849B
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 195450
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 135409
/ LENGTH: 283
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ US-09-270-849B-135409

Query Match 80.9%; Score 17.8; DB 16; Length 283;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGGCGCTCAG 22
Db 77 CCTTGGCGCTGGCGCTCCG 57

RESULT 13
US-09-540-210B-7050/c
/ Sequence 7050, Application US/09540210B
/ GENERAL INFORMATION:
/ APPLICANT: Sellhammer, Jeffrey J.
/ APPLICANT: Deleageane, Angelo M.
/ APPLICANT: Stuart, Susan G.
/ APPLICANT: Stuve, Laura L.
/ APPLICANT: Mullahy, Sara J.
/ APPLICANT: Naughton, Rebecca E.
/ TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
/ FILE REFERENCE: PD-1037 CIP
/ CURRENT APPLICATION NUMBER: US/09/540,210B
/ CURRENT FILING DATE: 2002-04-03
/ PRIOR APPLICATION NUMBER: 08/972,899
/ PRIOR FILING DATE: November 18, 1997
/ PRIOR APPLICATION NUMBER: 08/395,244
/ PRIOR FILING DATE: February 27, 1995
/ PRIOR APPLICATION NUMBER: 08/722,922
/ PRIOR FILING DATE: September 27, 1996
/ PRIOR APPLICATION NUMBER: 60/005,526
/ PRIOR FILING DATE: September 25, 1995
/ PRIOR APPLICATION NUMBER: 08/824,029
/ PRIOR FILING DATE: March 25, 1997
/ PRIOR APPLICATION NUMBER: 60/014,010
/ PRIOR FILING DATE: March 25, 1996
/ PRIOR APPLICATION NUMBER: 08/826,847
/ PRIOR FILING DATE: April 10, 1997
/ PRIOR APPLICATION NUMBER: 60/015,533
/ PRIOR FILING DATE: April 10, 1996
/ PRIOR APPLICATION NUMBER: 08/903,555
/ PRIOR FILING DATE: July 31, 1997
/ PRIOR APPLICATION NUMBER: 60/023,308
/ PRIOR FILING DATE: July 31, 1996
/ PRIOR APPLICATION NUMBER: 08/862,178
/ PRIOR FILING DATE: May 22, 1997
/ PRIOR APPLICATION NUMBER: 60/018,217
/ PRIOR FILING DATE: May 23, 1996
/ PRIOR APPLICATION NUMBER: 08/881,589
/ PRIOR FILING DATE: June 24, 1997
/ PRIOR APPLICATION NUMBER: 60/021,275
/ PRIOR FILING DATE: June 25, 1996
/ PRIOR APPLICATION NUMBER: 08/903,802
/ PRIOR FILING DATE: July 31, 1997
/ PRIOR APPLICATION NUMBER: 60/023,308
/ PRIOR FILING DATE: July 31, 1996
/ PRIOR APPLICATION NUMBER: 08/905,881
/ PRIOR FILING DATE: August 1, 1997
/ PRIOR APPLICATION NUMBER: 60/025,204
/ PRIOR FILING DATE: August 1, 1996
/ PRIOR APPLICATION NUMBER: 08/903,471
/ PRIOR FILING DATE: July 30, 1997
/ PRIOR APPLICATION NUMBER: 60/025,478
/ PRIOR FILING DATE: July 31, 1996
/ PRIOR APPLICATION NUMBER: 08/903,556
/ PRIOR FILING DATE: July 31, 1997
/ PRIOR APPLICATION NUMBER: 60/025,217
/ PRIOR FILING DATE: August 22, 1996
/ PRIOR APPLICATION NUMBER: 08/937,142
/ PRIOR FILING DATE: September 23, 1997
/ PRIOR APPLICATION NUMBER: 60/026,598
/ PRIOR FILING DATE: September 24, 1996
/ PRIOR APPLICATION NUMBER: 08/960,746
/ PRIOR FILING DATE: October 29, 1997
/ PRIOR APPLICATION NUMBER: 60/030,144
/ PRIOR FILING DATE: October 30, 1996
/ PRIOR APPLICATION NUMBER: 08/826,847
/ PRIOR FILING DATE: April 10, 1997
/ PRIOR APPLICATION NUMBER: 60/015,533
/ PRIOR FILING DATE: April 10, 1996
/ PRIOR APPLICATION NUMBER: 08/755,524
/ PRIOR FILING DATE: November 22, 1996
/ PRIOR APPLICATION NUMBER: 60/007,495
/ PRIOR FILING DATE: November 22, 1995
/ PRIOR APPLICATION NUMBER: 09/021,031
/ PRIOR FILING DATE: February 10, 1998
/ PRIOR APPLICATION NUMBER: 60/039,325
/ PRIOR FILING DATE: February 13, 1997
/ PRIOR APPLICATION NUMBER: 09/035,172
/ PRIOR FILING DATE: March 4, 1998
/ PRIOR APPLICATION NUMBER: 60/040,431
```

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; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0355P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 727:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: 2991071H1
; US-60-043-792-727

Query Match 80.9%; Score 17.8; DB 48; Length 283;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGCGCGCTGCGGCTCAG 22
   |||||
Db 47 CCTGCGCGCTGCGAGCCCGAG 27

RESULT 15
US-08-221-623A-3280/c
; Sequence 3280, Application US/08221623A
; GENERAL INFORMATION:
; APPLICANT: Adams, Mark D., et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression
; TITLE OF INVENTION: Products
; NUMBER OF SEQUENCES: 3319
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, &
; ADDRESSEE: Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 5.0
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221.623A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 325800-73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 994-1700
; TELEFAX: (201) 994-1744
; INFORMATION FOR SEQ ID NO: 3280:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-221-623A-3280

Query Match 80.9%; Score 17.8; DB 6; Length 301;

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us-09-270-437d-11.rnrm

Best Local Similarity 90.5%; Pred. NO. 2.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCTTGGCGGCTGCGGCTCA 21
Db 157 TCCTTGGCGGCTGCGGCTCA 137

Search completed: April 18, 2003, 09:35:44
Job time : 1214 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:28 ; Search time 245.167 Seconds
(without alignments)
400.770 Million cell updates/sec

Title: US-09-270-437D-11

Perfect score: 22
Sequence: 1 tccttgcgcgtcgccctcag 22

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5897297 seqs, 2233080881 residues

Total number of hits satisfying chosen parameters: 11794594

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*

- 1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US12_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US13_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US14_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US15_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US16_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	5	US-09-270-437D-11
2	22	100.0	1946	5	US-09-270-437D-7
3	22	100.0	12360069	5	US-09-948-128-318
4	17.8	80.9	139	6	US-09-513-999C-31413
5	17.8	80.9	301	6	US-09-912-293-219774
6	17.8	80.9	1006	1	PCT-US02-38821-19
7	17.4	79.1	1200	8	US-10-156-761-6708
8	17.4	79.1	15251	7	US-09-949-016-14274
9	17.2	78.2	341	6	US-09-912-293-44484
10	17.2	78.2	423	11	US-60-288-292-2261
11	17.2	78.2	1231	9	US-10-144-771-13059
12	17.2	78.2	1440	9	US-10-366-683-5799
13	17.2	78.2	1920	9	US-10-366-683-5851
14	17.2	78.2	2226	9	US-10-366-683-5851
15	17.2	78.2	1439395	5	US-09-948-128-252
16	17	77.3	609	9	US-10-366-683-10240
17	16.8	76.4	262	6	US-09-912-293-220875
18	16.8	76.4	340	7	US-09-837-604A-1013
19	16.8	76.4	424	7	US-09-837-604A-6577
20	16.8	76.4	468	11	US-60-141-233-62109
21	16.8	76.4	2959	1	PCT-US02-41414-1110
22	16.8	76.4	2976	8	US-10-363-616-152

c	23	16.8	76.4	6866	7	US-09-949-016-15807	Sequence 15807, A
	24	16.4	74.5	214	9	US-10-349-781-38057	Sequence 38057, A
	25	16.4	74.5	1568	9	US-10-144-771-4396	Sequence 4396, Ap
	26	16.4	74.5	1620	6	US-09-962-191A-25	Sequence 25, Appl
	27	16.4	74.5	1620	6	US-09-962-191-25	Sequence 25, Appl
c	28	16.4	74.5	1755	8	US-10-369-493-32171	Sequence 32171, A
	29	16.4	74.5	1755	6	US-09-989-733-180	Sequence 180, App
	30	16.4	74.5	1759	6	US-09-922-643-180	Sequence 180, App
	31	16.4	74.5	1759	9	US-10-125-923A-151	Sequence 151, App
	32	16.4	74.5	1759	9	US-10-205-892-151	Sequence 151, App
	33	16.4	74.5	1759	9	US-10-174-575A-151	Sequence 151, App
	34	16.4	74.5	1759	9	US-10-174-575A-151	Sequence 151, App
	35	16.4	74.5	1759	9	US-10-187-755-151	Sequence 151, App
	36	16.4	74.5	1759	9	US-10-187-749-151	Sequence 151, App
	37	16.4	74.5	1759	9	US-10-199-672-151	Sequence 151, App
	38	16.4	74.5	1759	9	US-10-194-486-151	Sequence 151, App
	39	16.4	74.5	1889	8	US-10-170-235-18030	Sequence 18030, A
	40	16.4	74.5	1889	6	US-09-980-7298-8	Sequence 8, Appl
	41	16.4	74.5	1935	8	US-10-170-235-26844	Sequence 26844, A
	42	16.4	74.5	1974	6	US-09-962-191A-24	Sequence 24, Appl
	43	16.4	74.5	1974	6	US-09-962-191-24	Sequence 24, Appl
c	44	16.2	73.6	208	6	US-09-513-999C-14079	Sequence 14079, A
	45	16.2	73.6	261	7	US-09-675-784A-871	Sequence 871, App

ALIGNMENTS

RESULT 1

US-09-270-437D-11
; Sequence 11, Application US/09270437D

; GENERAL INFORMATION:

; APPLICANT: Chen, Yao-Tseng

; APPLICANT: Gure, Ali

; APPLICANT: Teang, Solam

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Jager, Elke

; APPLICANT: Knuth, Alexander

; APPLICANT: Old, Lloyd J.

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen

; FILE REFERENCE: LUD 5538.1

; CURRENT APPLICATION NUMBER: US/09/270,437D

; CURRENT FILING DATE: 1999-03-16

; PRIOR FILING DATE: 09/061,709

; NUMBER OF SEQ ID NOS: 23

; SEQ ID NO 11

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

US-09-270-437D-11

Query Match 100.0%; Score 22; DB 5; Length 22;

Best Local Similarity 100.0%; Pred. No. 5.2;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCTTGGCGCTCGGCCTCAG 22

Db 1 TCCTTGGCGCTCGGCCTCAG 22

RESULT 2

US-09-270-437D-7

; Sequence 7, Application US/09270437D

; GENERAL INFORMATION:

; APPLICANT: Chen, Yao-Tseng

; APPLICANT: Gure, Ali

; APPLICANT: Teang, Solam

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Jager, Elke

; APPLICANT: Knuth, Alexander

APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens
FILE REFERENCE: LUD 538.1
CURRENT APPLICATION NUMBER: US/09/270,437D
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/061,709
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 7
LENGTH: 1946
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: CDS
LOCATION: 1622,1702,1771,1809,1833
OTHER INFORMATION: unsure of nucleotide
US-09-270-437D-7

Query Match 100.0%; Score 22; DB 5; Length 1946;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTTGGCGCTGGCGCTCAG 22
DB 38 TCCTTGGCGCTGGCGCTCAG 59

RESULT 3
US-09-948-128-318/c
Sequence 318, Application US/09948128
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
FILE REFERENCE: CL001294
CURRENT APPLICATION NUMBER: US/09/948,128
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 465
SEQ ID NO 318
LENGTH: 12360069
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(12360069)
OTHER INFORMATION: n = A,T,C or G
US-09-948-128-318

Query Match 100.0%; Score 22; DB 5; Length 12360069;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTTGGCGCTGGCGCTCAG 22
DB 10941150 TCCTTGGCGCTGGCGCTCAG 10941129

RESULT 4
US-09-513-999C-31413/c
Sequence 31413, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm

SEQ ID NO 31413
LENGTH: 139
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
LOCATION: 106
OTHER INFORMATION: s=g or c
US-09-513-999C-31413

Query Match 80.9%; Score 17.8; DB 6; Length 139;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGGCGCTCAG 22
DB 50 CCTTGGCGCTGGCGCTCAG 30

RESULT 5
US-09-912-293-219774/c
Sequence 219774, Application US/09912293
GENERAL INFORMATION:
APPLICANT: Rosen, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
FILE REFERENCE: PO-100
CURRENT APPLICATION NUMBER: US/09/912,293
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 08/103,744
PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 09/249,651
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 08/104,507
PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 08/196,363
PRIOR FILING DATE: 1994-02-15
PRIOR APPLICATION NUMBER: 09/859,490
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 08/196,362
PRIOR FILING DATE: 1994-02-15
PRIOR APPLICATION NUMBER: 08/221,623
PRIOR FILING DATE: 1994-03-31
PRIOR APPLICATION NUMBER: 08/220,691
PRIOR FILING DATE: 1994-03-31
PRIOR APPLICATION NUMBER: 09/741,830
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/813,155
PRIOR FILING DATE: 2001-03-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 244538
SEQ ID NO 219774
LENGTH: 301
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)...(9)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)...(14)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)...(16)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (25)...(25)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37)...(37)

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OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (42)..(42)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (59)..(59)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (61)..(61)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (91)..(91)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (104)..(104)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (126)..(126)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (263)..(263)
OTHER INFORMATION: n is equal to a,t,g, or c
US-09-912-293-219774
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Query Match      80.9%; Score 17.8; DB 6; Length 301;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 TCCTTGGCGCTCGGCTCA 21
Db 157 TCCTTGGCGCTCGGCTCA 137
```

```
RESULT 6
PCT-US02-38821-19/c
Sequence 19, Application PC/TUS0238821
GENERAL INFORMATION:
APPLICANT: Curagen Corp. et al.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
FILE REFERENCE: 24102-502D-061
CURRENT APPLICATION NUMBER: PCT/US02/38821
PRIOR FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: 60/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/381,495
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/401,788
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: 60/341,540
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/383,744
PRIOR FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/342,592
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/384,204
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/373,288
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/380,981
PRIOR FILING DATE: 2002-05-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Curaseq1ist version 0.1
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SEQ ID NO 19
LENGTH: 1006
TYPE: DNA
ORGANISM: CG164521-01
FEATURE:
NAME/KEY: CDS
LOCATION: (24)..(995)
PCT-US02-38821-19
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Query Match      80.9%; Score 17.8; DB 1; Length 1006;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 CCTTGGCGCTCGGCTCAG 22
Db 50 CCTTGGCGCTCGAGCCAG 30
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```
RESULT 7
US-10-156-761-6708/c
Sequence 6708, Application US/10156761
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6708
LENGTH: 1200
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1200)
US-10-156-761-6708
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Query Match      79.1%; Score 17.4; DB 8; Length 1200;
Best Local Similarity 94.7%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 TCCTTGGCGCTCGGCT 19
Db 668 TCCTTGGCGCTCGGCT 650
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```
RESULT 8
US-09-949-016-14274
Sequence 14274, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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us-09-270-437d-11.rnpn

Mon Apr 21 10:30:03 2003

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14274
; LENGTH: 15251
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14274

Query Match      79.1%; Score 17.4; DB 7; Length 15251;
Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTTGGCGGCTGGCGGCTC 20
DB 116 CCTTGGCGGCTGGCGGCTC 134

RESULT 9
US-09-912-293-44484/c
; Sequence 4484, Application US/09912293
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
; FILE REFERENCE: PO-100
; CURRENT APPLICATION NUMBER: US/09/912,293
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 08/103,744
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 09/249,651
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 08/104,507
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 08/196,363
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 09/859,490
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 08/196,362
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 08/221,623
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 08/220,691
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 09/741,830
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/813,155
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 244538
; SEQ ID NO 44484
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (236)..(236)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (257)..(257)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (280)..(280)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (285)..(285)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (326)..(326)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (333)..(333)
; OTHER INFORMATION: n is equal to a,t,g, or c
US-09-912-293-44484

Query Match      78.2%; Score 17.2; DB 6; Length 341;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGGCTCAG 22
DB 200 TCCTTGGCGGCTGGCGGCTCAG 179

RESULT 10
US-60-288-292-2261/c
; Sequence 2261, Application US/60288292
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Norris, Michael G
; TITLE OF INVENTION: Compounds isolated from forage plants
; TITLE OF INVENTION: and methods for their use.
; FILE REFERENCE: 1058P
; CURRENT APPLICATION NUMBER: US/60/288,292
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 49762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2261
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Lolium perenne
US-60-288-292-2261

Query Match      78.2%; Score 17.2; DB 11; Length 423;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGGCTCAG 22
DB 288 TCCTTGGCGGCTGGCGGCTCAG 267

RESULT 11
US-10-144-771-13059
; Sequence 13059, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CLO01321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 13059
; LENGTH: 1231
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-13059

Query Match      78.2%; Score 17.2; DB 9; Length 1231;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGGCTCAG 22
DB 357 TCCTTGGCGGCTGGCGGCTCAG 378

RESULT 12
US-10-366-683-5799
; Sequence 5799, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rubenfield, Marc J.
; APPLICANT: Nolling, Jork
; APPLICANT: Deloughery, Craig

```


; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/10/366,683
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5799
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-5799

Query Match 78.2%; Score 17.2; DB 9; Length 1440;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGCTCAG 22
|||||
DB 1301 TCCTTGGCGGCGGCTCCTCGG 1322

RESULT 13

US-10-366-683-5851/c
; Sequence 5851, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rubenfield, Marc J.
; APPLICANT: Nollings, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: PATH03-04
; CURRENT APPLICATION NUMBER: US/10/366,683
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5851
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-5851

Query Match 78.2%; Score 17.2; DB 9; Length 1920;
Best Local Similarity 86.4%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGCTCAG 22
|||||
DB 174 TCCTTGGCGGCGGCTCCTCGG 153

RESULT 14

US-10-366-683-5869/c
; Sequence 5869, Application US/10366683
; GENERAL INFORMATION:
; APPLICANT: Rubenfield, Marc J.
; APPLICANT: Nollings, Jork
; APPLICANT: Deloughery, Craig
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: PATH03-04
; CURRENT APPLICATION NUMBER: US/10/366,683
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 09/252,991
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5869
; LENGTH: 2226

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-5869

Query Match 78.2%; Score 17.2; DB 9; Length 2226;
Best Local Similarity 86.4%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGCTCAG 22
|||||
DB 143 TCCTTGGCGGCGGCTCCTCGG 122

RESULT 15

US-09-948-128-252/c
; Sequence 252, Application US/09948128
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
; FILE REFERENCE: CL001294
; CURRENT APPLICATION NUMBER: US/09/948,128
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 465
; SEQ ID NO 252
; LENGTH: 1439395
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1439395)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-128-252

Query Match 78.2%; Score 17.2; DB 5; Length 1439395;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGCTCAG 22
|||||
DB 1321142 TCATGAGCTTGGCGCTCAG 1321121

Search completed: April 18, 2003, 10:50:26
Job time : 3044.17 secs

GenCore version 5.1.4.p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic-- nucleic search, using sw model

Run on: April 18, 2003, 04:47:40 ; Search time 766 Seconds
(without alignments)
465.145 Million cell updates/sec

Title: US-09-270-437D-11

Perfect score: 22

Sequence: 1 tccttgccgcctgcggcctcag 22

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba:*

2: em_estum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hcc:*

9: gb_estl:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mue:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.4	83.6	1055	17	CNS01EYE
C 2	18.4	83.6	1128	17	BQ954241
C 3	18.4	83.6	1696	12	BF312525
C 4	17.8	80.9	250	9	AA591524
C 5	17.8	80.9	448	9	AA433531
C 6	17.8	80.9	461	10	AW052407

C 7	17.8	80.9	490	12	BG465076
C 8	17.8	80.9	512	10	AV433340
C 9	17.8	80.9	708	12	BE254482
C 10	17.8	80.9	767	12	BG699633
C 11	17.8	80.9	856	9	AL519496
C 12	17.8	80.9	905	9	AL528423
C 13	17.8	80.9	936	17	CNS035RV
C 14	17.8	80.9	938	14	BQ684757
C 15	17.8	80.9	961	12	BG617183
C 16	17.8	80.9	1013	12	BG757407
C 17	17.4	79.1	432	9	AA120169
C 18	17.4	79.1	862	13	BI818151
C 19	17.2	78.2	291	9	AL825604
C 20	17.2	78.2	319	12	BF886876
C 21	17.2	78.2	367	10	BB843150
C 22	17.2	78.2	382	10	BB842521
C 23	17.2	78.2	437	10	BB864106
C 24	17.2	78.2	460	9	AA000295
C 25	17.2	78.2	497	17	BH035572
C 26	17.2	78.2	508	10	BB858287
C 27	17.2	78.2	512	10	BE544739
C 28	17.2	78.2	546	10	AW210189
C 29	17.2	78.2	552	12	BG086730
C 30	17.2	78.2	552	14	BQ606886
C 31	17.2	78.2	594	17	AZ879071
C 32	17.2	78.2	597	12	BF719752
C 33	17.2	78.2	600	12	BG086847
C 34	17.2	78.2	603	10	BB630902
C 35	17.2	78.2	613	17	BH886739
C 36	17.2	78.2	620	9	AA797109
C 37	17.2	78.2	623	13	BI077950
C 38	17.2	78.2	644	10	BB613343
C 39	17.2	78.2	644	10	BE291303
C 40	17.2	78.2	672	13	BI659501
C 41	17.2	78.2	705	10	BE414309
C 42	17.2	78.2	710	12	BF786998
C 43	17.2	78.2	713	17	BH577830
C 44	17.2	78.2	776	17	AQ745151
C 45	17.2	78.2	800	17	CNS06YME

ALIGNMENTS

RESULT 1	CNS01EYE/c	1055 bp	DNA	linear	GSS 30-MAY-2001
LOCUS	Anopheles gambiae GSS SP6 end of clone 03E18 of NotreDame1 library				
DEFINITION	from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.				
ACCESSION	AL141159				
VERSION	AL141159.1				GI:6999277
KEYWORDS	GSS:				
SOURCE	African malaria mosquito.				
ORGANISM	Anopheles gambiae				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.				
REFERENCE	1 (bases 1 to 1055)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
REFERENCE	2 (bases 1 to 1055)				
AUTHORS	Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France				
COMMENT	This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.				

```

FEATURES
source
Location/Qualifiers
1. 1055
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="03E18"
/notes="end : SP6"
BASE COUNT 244 a 230 c 255 g 320 t 6 others
ORIGIN
Query Match 83.6%; Score 18.4; DB 17; Length 1055;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTTGGCGGCTGGCGCTCA 21
|||||
Db 262 CCTTGGCGGCTGGCGCTCA 243
|||||

RESULT 2
BQ954241 1128 bp mRNA linear EST 21-AUG-2002
AGENCOURT 864349 lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6197933 5', mRNA sequence.
ACCESSION BQ954241
VERSION BQ954241.1 GI:22369719
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1128)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remai.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13608 row: m column: 06
High quality sequence stop: 338.
FEATURES
source
Location/Qualifiers
1. 1128
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6197933"
/clone_lib="Lupski_sciatic_nerve"
/sex="male"
/tissue type="sciatic nerve"
/dev stage="adult, 70 yr"
/lab host="DH10B"
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dt priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACTAGTTCATCGAGCGCGCTCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
BASE COUNT 296 a 324 c 322 g 186 t
ORIGIN
Query Match 83.6%; Score 18.4; DB 14; Length 1128;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FEATURES
source
Location/Qualifiers
1. 1055
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="03E18"
/notes="end : SP6"
BASE COUNT 244 a 230 c 255 g 320 t 6 others
ORIGIN
Query Match 83.6%; Score 18.4; DB 17; Length 1055;
Best Local Similarity 95.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGCTC 20
|||||
Db 629 TCCTTGGCGGCTGGCGCTC 648
|||||

RESULT 3
B312525/c 1696 bp mRNA linear EST 21-NOV-2000
LOCUS B312525
DEFINITION B01897489F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126750 5',
mRNA sequence.
ACCESSION B312525
VERSION B312525.1 GI:11260337
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1696)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remai.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1017 row: a column: 23
High quality sequence stop: 169.
FEATURES
source
Location/Qualifiers
1. 1696
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4126750"
/clone_lib="NIH_MGC_19"
/tissue type="neuroblastoma"
/lab host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pOTS7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 420 a 395 c 535 g 346 t
ORIGIN
Query Match 83.6%; Score 18.4; DB 12; Length 1696;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCTTGGCGGCTGGCGCTC 20
|||||
Db 1315 TCCTTGGCGGCTGGCGCTC 1296
|||||

RESULT 4
AA591524/c 250 bp mRNA linear EST 16-SEP-1997
LOCUS AA591524
DEFINITION vk23e01.r1 Knowles Solter mouse blastocyst B1 Mus musculus CDNA
clone IMAGE:947448 5', mRNA sequence.
ACCESSION AA591524
VERSION AA591524.1 GI:2404837
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 250)

```

AUTHORS

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE
JOURNAL
COMMENT

The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:544304

Putative full length read
vector to vector length is 251.

FEATURES
source

Location/Qualifiers
1. .250

/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:947448"
/clone_lib="Knowles Solter mouse blastocyst B1"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH108"
/note="Organ: embryo; Vector: pSPORT; Site_1: NotI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: SalI(dT): 5'-CGTGCACGCTGCGCTTTT-3'. cDNAs were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger inserts) and B3."

BASE COUNT
ORIGIN

55 a 80 c 82 g 33 t

Query Match 80.9%; Score 17.8; DB 9; Length 250;
Best Local Similarity 90.5%; Pred. NO. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGCGGCTCAG 22
|||
Db 151 CCTTGGCGCTGCGGCTCAG 131

RESULT 5
AA433531/c

LOCUS
DEFINITION
vfa3a06.r1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:846514
5', mRNA sequence.

ACCESSION
VERSION
AA433531.1 GI:2138449

KEYWORDS
SOURCE

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 448)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

FEATURES

source

Location/Qualifiers
1. .448
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:846514"
/clone_lib="Soares mouse NBMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH108"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAAGTGGAGCGCGCGAAGTTT-3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Patima Bonaudo."

BASE COUNT
ORIGIN

90 a 143 c 115 g 100 t

Query Match 80.9%; Score 17.8; DB 9; Length 448;
Best Local Similarity 90.5%; Pred. NO. 1.8e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGCGGCTCAG 22
|||
Db 210 CCATGCGCTGCGGCTCAG 190

RESULT 6
AW052407/c

LOCUS
DEFINITION

rs35b02.y1 Sommer Pristionchus Pristionchus pacificus cDNA 5', similar to SM:MYSA_CAEEL P12844 MYOSIN HEAVY CHAIN A i, mRNA sequence.

AW052407

AW052407.1 GI:5914766

EST.

Pristionchus pacificus.

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

1 (bases 1 to 461)

McCarte,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,

Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,

Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.,

Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,

M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,

Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and

Wilson,R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

The library was constructed by Dr. Ralf Sommer DNA Sequencing by:

Washington University Genome Sequencing Center

Contact Dr. Ralf Sommer (ralf.sommer@wustl.edu) for

Mon Apr 21 10:30:04 2003

information about this clone.
Seq primer: -40RP from Gibco
High quality sequence stop: 414.

FEATURES source

1. .461
/organism="Pristionchus pacificus"
/strain="PS 312"
/db_xref="taxon:54126"
/clone_lib="Sommer Pristionchus"
/sex="predominantly hermaphroditic"
/dev_stage="mixed stages (embryo to adult)"
/lab_host="not applicable (host cell line)"
/note="vector: Uni-ZAP XR Vector (Stratagene); Site_1: 5'
ECORI; Site_2: 3' XhoI; 1st strand cDNA was primed with a
XhoI - oligo(dT) primer. Double-stranded cDNA was ligated
to EcoRI adaptors digested with XhoI and cloned into XhoI
and EcoRI sites. Primary complexity of the library was 10
in the 7th. The library went through one round of
amplification."

BASE COUNT 135 a 118 c 154 g 54 t

Query Match 80.9%; Score 17.8; DB 10; Length 461;
Best Local Similarity 90.5%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGGCGCTCAG 22
|||||
DB 217 CCTTGGCGCTGGCGCTCAG 197

RESULT 7
BG465076/c 490 bp mRNA linear EST 20-MAR-2001
LOCUS EMI_33_A11.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA

DEFINITION BG465076
sequence.
ACCESSION BG465076
VERSION BG465076.1 GI:13393954
KEYWORDS EST.
SOURCE Sorghum bicolor

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 490)
Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.
An EST database from Sorghum: developing embryos
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 484
POLYA=No.

Location/Qualifiers

1. 490
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
74 a 199 c 178 g 38 t 1 others

BASE COUNT

Query Match 80.9%; Score 17.8; DB 12; Length 490;
Best Local Similarity 90.5%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGGCGCTCAG 22
|||||
DB 345 CCTTGGCGCTGGCGCTCAG 325

FEATURES source

1. 512
/organism="Porphyriza yezoensis"
/strain="TU-1"
/db_xref="taxon:2788"
/clone_lib="PM027e05"
/clone_lib="Porphyriza yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 106 a 159 c 154 g 93 t
ORIGIN
Query Match 80.9%; Score 17.8; DB 10; Length 512;
Best Local Similarity 90.5%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGGCGCTCAG 22
|||||
DB 212 CCTTGGCGCTGGCGCTCAG 232

RESULT 9
BE254482/c 708 bp mRNA linear EST 13-JUL-2000
LOCUS 60111575F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352314 5',
DEFINITION mRNA sequence.
ACCESSION BE254482
VERSION BE254482.1 GI:9124910
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 708)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

BASE COUNT 106 a 159 c 154 g 93 t
ORIGIN
Query Match 80.9%; Score 17.8; DB 10; Length 512;
Best Local Similarity 90.5%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTTGGCGCTGGCGCTCAG 22
|||||
DB 212 CCTTGGCGCTGGCGCTCAG 232

RESULT 9
BE254482/c 708 bp mRNA linear EST 13-JUL-2000
LOCUS 60111575F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352314 5',
DEFINITION mRNA sequence.
ACCESSION BE254482
VERSION BE254482.1 GI:9124910
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 708)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCW151 row: e column: 19
 High quality sequence stop: 588.
 Location/Qualifiers
 1..708

FEATURES

source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3352314"
 /clone_lib="NIH_MGC_16"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pORF7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 236 a 159 c 188 g 125 t
 ORIGIN

Query Match 80.9%; Score 17.8; DB 10; Length 708;
 Best Local Similarity 90.5%; Pred. No. 1.9e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CCTTGGCGCTGGCGGCTCAG 22
 |||||
 Db 551 CCTTGGCGCTGGCGGCTCAG 531

RESULT 10
 BG599633/c
 LOCUS
 DEFINITION 602679365F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4811824 5',
 mRNA sequence.
 ACCESSION BG599633
 VERSION BG599633.1 GI:13968143
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 767)
 NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein (NHGRI), Shiraki
 cDNA Library Preparation: Miklos Palkovits, M.D., Ph.D.
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10703 row: b column: 17
 High quality sequence stop: 616.
 Location/Qualifiers
 1..767

FEATURES

source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4811824"
 /clone_lib="NIH_MGC_95"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gcgcag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
 size-selected for average insert size 2.5 kb and
 normalized to ROT 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
 BASE COUNT 156 a 259 c 242 g 110 t
 ORIGIN

Query Match 80.9%; Score 17.8; DB 12; Length 767;
 Best Local Similarity 90.5%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CCTTGGCGCTGGCGGCTCAG 22
 |||||
 Db 53 CCTTGGCGCTGGCGGCTCAG 33

RESULT 11
 AL519496/c
 LOCUS
 DEFINITION AL519496 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB004Y122 5
 prime, mRNA sequence.
 ACCESSION AL519496
 VERSION AL519496.1 GI:12782989
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 856)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1..856

source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DB004Y122"
 /clone_lib="LTI_NFL004_NBC2"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact : Feng Liang Life
 Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : fliang@life.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 169 a 289 c 257 g 139 t
 ORIGIN

Query Match 80.9%; Score 17.8; DB 9; Length 856;
 Best Local Similarity 90.5%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CCTTGGCGCTGGCGGCTCAG 22
 |||||
 Db 26 CCTTGGCGCTGGCGGCTCAG 6

RESULT 12
 AL528423/c

Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*

Unpublished
3 (bases 1 to 936)
Genoscope.
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the *Tetraodon nigroviridis* genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
Location/Qualifiers
1..936
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="214809"
/clone_lib="G"
/note="Genoscope sequence ID : COAG214CA05SP1-end : PUC-ori"

BASE COUNT 247 a 204 g 190 G 276 t 19 others
ORIGIN

Query Match 80.9%; Score 17.8; DB 17; Length 936;
Best Local Similarity 90.5%; Pred: No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCTTGGCGCTGGCGCTCA 21
|||||
DB 33 TCCTTGGCGCTGGCGCCACA 53
|||||

RESULT 14
B0684757/c
LOCUS
DEFINITION B0684757 938 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8343533 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250259
5', mRNA sequence.
ACCESSION B0684757
VERSION B0684757.1 GI:21810073
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 938)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: ATCC
cDNA library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2393 row: a column: 12
High quality sequence stop: 710.
Location/Qualifiers
1..938
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6250259"
/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University

LOCUS AL528423 905 bp mRNA linear EST 13-FEB-2001
DEFINITION AL528423 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC029YH22 5
prime, mRNA sequence.

ACCESSION AL528423
VERSION AL528423
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 905)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrat@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
FEATURES
source 1..905
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC029YH22"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(GT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 183 a 302 c 273 g 145 t 2 others
ORIGIN
Query Match 80.9%; Score 17.8; DB 9; Length 905;
Best Local Similarity 90.5%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
Matches 19; Conservative
Qy 2 CCTTGGCGCTGGCGGCTCTAG 22
|||||
Db 35 CCTTGGCGCTGGCGGCTCTAG 15
|||||
RESULT 13
CNS035RV
LOCUS
DEFINITION CNS035RV 936 bp DNA linear GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
214B09 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL229108
VERSION AL229108.1 GI:7888103
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 936)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissensbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
JOURNAL Tetraodon nigroviridis
REFERENCE 2 (bases 1 to 936)
AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
TITLE Tetraodon nigroviridis

of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 190 a 317 c 285 g 146 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 14; Length 938;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTTGGCGGCTGGCGGCTCAG 22
|||||
Db 26 CCTTGGCGGCTGGCGGCTCAG 6
|||||

RESULT 15
BG617183/c
LOCUS
DEFINITION BG617183 961 bp mRNA linear EST 18-APR-2001
602615581F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4734237 5',
mRNA sequence.
ACCESSION BG617183
VERSION BG617183
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 961)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM1597 row: a column: 22
High quality sequence stop: 211.

FEATURES
source
1..961
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4734237"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pDNR-LJB (Clontech); Site 1:
SfiI (ggcgcctcgcc); Site 2: SfiI (ggccataggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCATTTGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGCCCGGGGGCGGCGGCTCAG-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

BASE COUNT 253 a 216 c 408 g 84 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 12; Length 961;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCTTGGCGGCTGGCGGCTCA 21
|||||
Db 704 TCCTTGGCGGCTGGCGGCTCA 684
|||||

Search completed: April 18, 2003, 07:31:53
Job time : 770.167 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:46:26 ; Search time 305.273 Seconds
(without alignments)
2192.677 Million cell updates/sec

Title: US-09-270-437D-12

Perfect score: 23
Sequence: 1 ccaactgggtggccattcagcttc 23

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_in:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rdt:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	23	100.0	1708	6	AR171864	AR171864 Sequence
C 2	23	100.0	1946	6	AR171866	AR171866 Sequence
C 3	23	100.0	2130	9	AF117106	AF117106 Homo sapi
C 4	23	100.0	2381	9	AF198254	AF198254 Homo sapi
C 5	23	100.0	65435	2	AC104587	AC104587 Homo sapi
C 6	23	100.0	147767	2	AC105030	AC105030 Homo sapi
C 7	23	100.0	154604	2	AC104974	AC104974 Homo sapi
C 8	23	100.0	159122	2	AC025556	AC025556 Homo sapi
C 9	23	100.0	168613	9	AC091133	AC091133 Homo sapi
C 10	19.8	86.1	299350	1	AP005370	AP005370 Thermosyn
C 11	19.4	84.3	54441	2	AC101033	AC101033 Mus muscu
C 12	19.4	84.3	54441	2	AC101033	AC101033 Mus muscu
C 13	19.4	84.3	191918	2	AC102692	AC102692 Mus muscu
C 14	19.4	84.3	277892	2	AC125105	AC125105 Mus muscu
C 15	18.8	81.7	1520	9	BC013150	BC013150 Homo sapi
C 16	18.8	81.7	1648	9	BC015866	BC015866 Homo sapi
C 17	18.8	81.7	2526	3	AY052019	AY052019 Drosophill
C 18	18.8	81.7	3098	9	AK091249	AK091249 Homo sapi
C 19	18.8	81.7	14668	2	AC018286	AC018286 Drosophill
C 20	18.8	81.7	149433	9	AL135901	AL135901 Human DNA
C 21	18.8	81.7	152443	3	AC009208	AC009208 Drosophill
C 22	18.8	81.7	179191	2	AL808114	AL808114 Mus muscu
C 23	18.8	81.7	181542	9	AL137019	AL137019 Human DNA
C 24	18.8	81.7	182494	3	AC009343	AC009343 Drosophill
C 25	18.8	81.7	205336	10	AC116576	AC116576 Mus muscu
C 26	18.8	81.7	226950	10	AL671011	AL671011 Mouse DNA
C 27	18.8	81.7	257909	3	AE003828	AE003828 Drosophill
C 28	18.4	80.0	131145	9	HSR277661	HSR277661 Homo sapi
C 29	18.4	80.0	168097	2	AC102401	AC102401 Mus muscu
C 30	18.4	80.0	174986	9	HSR277662	HSR277662 Homo sapi
C 31	18.4	80.0	213873	2	AC019200	AC019200 Homo sapi
C 32	18.4	80.0	223741	9	AC091013	AC091013 Homo sapi
C 33	18.2	79.1	10918	1	AE013239	AE013239 Methanosa
C 34	18.2	79.1	11562	1	AE009689	AE009689 Brucella
C 35	18.2	79.1	133451	9	AL158847	AL158847 Human DNA
C 36	18.2	79.1	145327	9	AP004285	AP004285 Homo sapi
C 37	18.2	79.1	152760	2	AC106146	AC106146 Rattus no
C 38	18.2	79.1	155704	9	AC073330	AC073330 Homo sapi
C 39	18.2	79.1	156461	9	AC004383	AC004383 Human Chr
C 40	18.2	79.1	168140	2	AC013379	AC013379 Homo sapi
C 41	18.2	79.1	168949	9	AC046134	AC046134 Homo sapi
C 42	18.2	79.1	175882	2	AC118532	AC118532 Rattus no
C 43	18.2	79.1	176128	2	AC124533	AC124533 Mus muscu
C 44	18.2	79.1	178388	9	AC079630	AC079630 Homo sapi
C 45	18.2	79.1	178588	2	AC118834	AC118834 Rattus no

ALIGNMENTS

RESULT 1
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LOCUS AR171864 Sequence 5 from patent US 6297364.
DEFINITION AR171864 1708 bp DNA linear PAT 17-DEC-2001
ACCESSION AR171864
VERSION AR171864.1 GI:17910814
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1708)
AUTHORS Chen, Y.-T., Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K.
and Old, L.J.
TITLE Isolated nucleic acid molecule encoding cancer associated antigen,
the antigen itself, and uses thereof

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JOURNAL Patent: US 6297364-A 5 02-OCT-2001;
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QY 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 68 CCAACTGGTGGCCATTGAGCTTC 46

RESULT 2
LOCUS AR171866/c 1946 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6297364.
ACCESSION AR171866
VERSION AR171866.1 GI:17910816
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1946)
AUTHORS Chen,Y.-F., Gure,A., Tsang,S., Stockert,E., Jager,E., Alexander,K.
and Old,D.J.
TITLE Isolated nucleic acid molecule encoding cancer associated antigen,
the antigen itself, and uses thereof
JOURNAL Patent: US 6297364-A 7 02-OCT-2001;
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DEFINITION Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete
cds.
ACCESSION AF117106
VERSION AF117106.1 GI:4191607
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2130)
AUTHORS Nielsen,J., Christensen,J., Lykke-Andersen,J., Johnsen,A.H.,
Wewer,U.M. and Nielsen,F.C.
TITLE A family of insulin-like growth factor II mRNA-binding proteins
represses translation in late development
JOURNAL Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
MEDLINE 99108099
PUBMED 9891060
REFERENCE 2 (bases 1 to 2130)
AUTHORS Nielsen,J., Christensen,J., Lykke-Andersen,J., Johnsen,A.H.,
Wewer,U.M. and Nielsen,F.C.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark

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DEFINITION Homo sapiens mRNA-binding protein CRDBP mRNA, complete cds.
ACCESSION AF198254
VERSION AF198254.1 GI:7141071
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2381)
AUTHORS Ioannidis,P., Trangas,T., Dimitriadis,E., Samiotaki,M.,
Panoussakopoulos,G., Kyriazoglou,I., Voutzoulis,S.,
Tsiapalis,C.M., Kittas,C., Agnantis,N. and Pandis,N.
TITLE Ectopic expression of a KH-domain containing protein, highly
homologous to both human IMP-1 and mouse CRD-BP, in benign and
malignant mesenchymal tumors
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2381)
AUTHORS Ioannidis,P., Trangas,T., Dimitriadis,E. and Samiotaki,M.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-1999) G. Papanikolaou Research Center, St Savvas
Hospital, 171 Alexandras Avenue, Athens, Attica 11522, Greece
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596 a 687 c 664 g 434 t

Query Match 100.0%; Score 23; DB 9; Length 2381;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Homo sapiens chromosome 17 clone RP11-78C17 map 17, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
ACCESSION AC104587
VERSION AC104587.1 GI:17646987
KEYWORDS HTG; HTGS PHASE0.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-78C17
Unpublished
2 (bases 1 to 65435)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepep,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
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Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testfay,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,K., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (13-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

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Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L22859
Center clone name: 78_C_17
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* NOTE: This record contains 84 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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Mon Apr 21 10:30:06 2003

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RESULT 6

AC105030

LOCUS

DEFINITION

AC105030

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

AC105030 147767 bp DNA linear HTG 06-AUG-2002
Homo sapiens chromosome 17 clone CTD-2244F11 map 17, *** SEQUENCING
IN PROGRESS ***, 3 ordered pieces.

AC105030

AC105030.4 GI:22123404

HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Plrimates; Catarrhini; Homnidae; Homo.

Birren,B., Nusbaum,C. and Lander,E.

1 (bases 1 to 147767)

Homo sapiens chromosome 17, clone CTD-2244F11

Unpublished

2 (bases 1 to 147767)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,

Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,

Choepl,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,

Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,

Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,

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Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (22-DEC-2001) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 147767)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,

Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,

Camarata,J., Chang,J., Chazaro,B., Choepl,Y., Collymore,A.,

Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,

Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,

Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,

Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,

Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,

McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mieng,V.,

Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,

O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 6, 2002 this sequence version replaced gi:21426162.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L23011
Center clone name: 2244_F_11

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 64310: contig of 64310 bp in length
* 64311 64410: gap of 100 bp
* 64411 86773: contig of 22363 bp in length
* 86774 86873: gap of 100 bp
* 86874 147767: contig of 60894 bp in length.

FEATURES source

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/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="CTD-2244F11"
/clone_lib="CITDI Human BAC"
BASE COUNT 41792 a 34009 c 33361 g 38110 t 495 others

ORIGIN

Query Match 100.0%; Score 23; DB 2; Length 147767;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCAACTGGTGGCCATTCAGCTTC 23

Db 106124 CCAACTGGTGGCCATTCAGCTTC 106146

RESULT 7

AC104974/c
LOCUS AC104974 154604 bp DNA linear HTG 13-FEB-2002
DEFINITION Homo sapiens chromosome 17 clone RP11-145L16 map 17, WORKING DRAFT
SEQUENCE, 23 ordered pieces.
AC104974
VERSION AC104974.3 GI:18653683
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154604)

REFERENCE AUTHORS TITLE JOURNAL

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-145L16
Unpublished

REFERENCE AUTHORS

2 (bases 1 to 154604)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campion, A., Chang, J., Chazaro, B., Choquel, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferrel, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Milnova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 13, 2002 this sequence version replaced gi:18464184.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L22871

Center clone name: 145_L16

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 148031 bases at least Q40
Consensus quality: 150405 bases at least Q30
Consensus quality: 151462 bases at least Q20
Insert size: 146000; agarose-fp
Insert size: 152404; sum-of-contigs
Quality coverage: 9.3 in Q20 bases; agarose-fp
Quality coverage: 8.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 1709: contig of 1709 bp in length
* 1710 1809: gap of 100 bp
* 1810 1999: contig of 190 bp in length
* 2000 2099: gap of 100 bp
* 2100 3127: contig of 1028 bp in length
* 3128 3227: gap of 100 bp
* 3228 4561: contig of 1334 bp in length
* 4562 4661: gap of 100 bp
* 4662 5811: contig of 1150 bp in length
* 5812 5911: gap of 100 bp
* 5912 7151: contig of 1240 bp in length
* 7152 7251: gap of 100 bp
* 7252 8261: contig of 1010 bp in length
* 8262 8361: gap of 100 bp

* 8362 9739: contig of 1378 bp in length
* 9740 9839: gap of 100 bp
* 9840 12105: contig of 2266 bp in length
* 12106 12205: gap of 100 bp
* 12206 35760: contig of 23555 bp in length
* 35761 35860: gap of 100 bp
* 35861 38000: contig of 2140 bp in length
* 38001 38100: gap of 100 bp
* 38101 41369: contig of 3269 bp in length
* 41370 41459: gap of 100 bp
* 41470 44094: contig of 2625 bp in length
* 44095 44194: gap of 100 bp
* 44195 47400: contig of 3206 bp in length
* 47401 47500: gap of 100 bp
* 47501 53741: contig of 6241 bp in length
* 53742 53841: gap of 100 bp
* 53842 60833: contig of 6992 bp in length
* 60834 60933: gap of 100 bp
* 60934 72421: contig of 11488 bp in length
* 72422 72521: gap of 100 bp
* 72522 84887: contig of 12366 bp in length
* 84888 84987: gap of 100 bp
* 84988 99600: contig of 14613 bp in length
* 99601 99700: gap of 100 bp
* 99701 115353: contig of 15653 bp in length
* 115354 115453: gap of 100 bp
* 115454 131255: contig of 15802 bp in length
* 131256 131355: gap of 100 bp
* 131356 152505: contig of 21150 bp in length
* 152506 152605: gap of 100 bp
* 152606 154604: contig of 1999 bp in length.

FEATURES

source

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/map="17"
/clone_lib="RPC1-II Human Male BAC"

1. 1709
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clone_end:SP6
vector_side:left"

1810. 1999
/note="assembly_fragment"
2100. 3127
/note="assembly_fragment"
3228. 4561
/note="assembly_fragment"
4562. 5811
/note="assembly_fragment"
5912. 7151
/note="assembly_fragment"
7252. 8261
/note="assembly_fragment"
8362. 9739
/note="assembly_fragment"
9840. 12105
/note="assembly_fragment"
12206. 35760
/note="assembly_fragment"
35861. 38000
/note="assembly_fragment"
38101. 41369
/note="assembly_fragment"
41470. 44094
/note="assembly_fragment"
44195. 47400
/note="assembly_fragment"
47501. 53741
/note="assembly_fragment"
53842. 60833
/note="assembly_fragment"

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misc_feature 152606. 154604
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clone_end:T7
vector_side:right"

BASE COUNT 42238 a 34832 c 34671 g 40661 t 2202 others
ORIGIN

Query Match 100.0%; Score 23; DB 2; Length 154604;
Best Local Similarity 100.0%; Pred.No. 1.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTACGCTTC 23
|||||
DB 133577 CCAACTGGTGGCCATTACGCTTC 133555

RESULT 8

AC025556

LOCUS

DEFINITION

SEQUENCE, 17 unordered pieces.

AC025556

VERSION

HTG; HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

COMMENT

AC025556 159122 bp DNA linear HTG 01-SEP-2000
Homo sapiens chromosome 17 clone RP11-501C14, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
AC025556
AC025556.4 GI:9958273
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
Waterston,R.H.
2 (bases 1 to 159122)
Direct Submission
Submitted (10-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:8570253.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0501C14
----- Summary Statistics -----
Sequencing vector: M13; 96%
Chemistry: Dye-primer ET; 96% of reads
Chemistry: Dye-terminator Big Dye; 4% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 148686 bases at least Q40
Consensus quality: 152251 bases at least Q30
Consensus quality: 154277 bases at least Q20
Insert size: 181000; agarose-fp
Insert size: 157522; sum-of-contigs
Quality coverage: 3.86 in Q20 bases; agarose-fp
Quality coverage: 4.48 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 17 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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1 7635: contig of 7635 bp in length
* 7636: gap of unknown length
* 7736: contig of 7745 bp in length
* 15480: gap of unknown length
* 15581: gap of 9509 bp in length
* 25089: gap of unknown length
* 25090: contig of 9817 bp in length
* 25190: gap of unknown length
* 35007: gap of unknown length
* 35107: contig of 9403 bp in length
* 44509: gap of unknown length
* 44510: contig of 11992 bp in length
* 46610: gap of unknown length
* 56601: contig of 11992 bp in length
* 56702: gap of unknown length
* 64536: contig of 7835 bp in length
* 64637: gap of unknown length
* 79941: contig of 15305 bp in length
* 80041: gap of unknown length
* 95746: contig of 15705 bp in length
* 95846: gap of unknown length
* 125332: contig of 29686 bp in length
* 125333: gap of unknown length
* 126811: contig of 1179 bp in length
* 126911: gap of unknown length
* 126912: contig of 2235 bp in length
* 129146: gap of unknown length
* 129147: contig of 3446 bp in length
* 1329247: contig of 3446 bp in length
* 132693: gap of unknown length
* 132792: gap of unknown length
* 135914: contig of 3122 bp in length
* 135915: gap of unknown length
* 136014: gap of unknown length
* 143560: contig of 7546 bp in length
* 143661: gap of unknown length
* 150766: contig of 7106 bp in length
* 150767: gap of unknown length
* 150867: contig of 8256 bp in length.
  
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FEATURES

source

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misc_feature

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misc_feature

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misc_feature

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misc_feature

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64637. .79941
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misc_feature

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80042. .95746
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misc_feature

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95847. .125532
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misc_feature

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  143661. .150766
  /note="assembly_name:Contig8"
  150867. .159122
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Query Match      100.0%; Score 23; DB 2; Length 159122;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  
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Db 67199 CCAACTGGTGGCCATTGAGCTTC 67221
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RESULT 9

AC091133

LOCUS

DEFINITION

AC091133

ACCESSION

AC091133.11

KEYWORDS

HTG.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 168613)

Birren,B., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 17, clone RP11-501C14

Unpublished

2 (bases 1 to 168613)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,

Barna,N., Bastien,V., Bouguelavsky,L., Boukhalter,B., Brown,A.,

Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,

Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K.,

Diaz,J.S., Dodge,S., Faros,S., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,

Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,

Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,

Maclean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,

Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,

Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,

Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,

Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,

Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,

Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,

Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S.,

Theodorovic,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (01-APR-2001) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 168613)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Bloom,T., Bouguelavsky,L.,

Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,

Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,

Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Faros,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,

Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,

Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,

Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N.,

Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J.,

Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,

TITLE	JOURNAL	REFERENCE	AUTHORS
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., PhunKhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, K., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	Direct Submission	Submitted (17-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
4 (bases 1 to 168613)			
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, F., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., PhunKhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	Direct Submission	Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
On Jul 1, 2002 this sequence version replaced gi:21431160.			
All repeats were identified using RepeatMasker:			
Smit, A.F.A. & Green, P. (1996-1997)			
http://ftp.genome.washington.edu/RM/RepeatMasker.html			
----- Genome Center			
Center: Whitehead Institute/ MIT Center for Genome Research			
Center code: WIBR			
Web site: http://www-seq.wi.mit.edu			
Contact: sequence_submissions@genome.wi.mit.edu			
----- Project Information			
Center project name: L12028			
Center clone name: 501_C_14			
----- Location/Qualifiers			
1. 168613			
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ACCESSION AC101033
VERSION AC101033.1 GI:17059807
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-8514
Unpublished
2 (bases 1 to 54441)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
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Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
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Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L14840
Center clone name: 85_I_4

* NOTE: This record contains 68 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
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* identifying clones that may be gene-rich and allows
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* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
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FEATURES

source

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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 12

AC101033/c

Mon Apr 21 10:30:06 2003

AC101033 54441 bp DNA linear HTG 23-NOV-2001
Mus musculus clone RP23-8514, LOW-PASS SEQUENCE SAMPLING.
AC101033
AC101033.1 GI:17059807
HTG; HTGS PHASE0.
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Birren, B., Linton, L., Nussbaum, C. and Lander, E.
1 (bases 1 to 54441)
Mus musculus, clone RP23-8514
Unpublished
2 (bases 1 to 54441)
Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L14840
Center clone name: 85_I_4

* NOTE: This record contains 68 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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* 790 1570: contig of 781 bp in length
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ORGANISM
Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 1 (bases 1 to 191918)
 Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP24-49IK18
 Unpublished
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 Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 191918)
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhaltier,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
 Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Fero,S., Ferreira,P., Fitzhugh,W., Gage,D., Galign,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B.,
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
 Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
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 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
 Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
 Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 21, 2002 this sequence version replaced gi:17060802.
 All repeats were identified using RepeatMasker.
 Smit, A.P.A. & Green, P. (1996-1997)

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D_b 38305 AAATGGTGGCCATTGAGCTTC 38285

AC102692
LOCUS

ACCESSION

SOURCE

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/note="Assembly Fragment"

BASE COUNT      58327 a 40328 c 39648 g 52315 t 1300 others
ORIGIN

Query Match      84.3%; Score 19.4; DB 2; Length 191918;
Best Local Similarity 95.2%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 1; Indels 0;

QY      3 AACTGGTGGCCATTTCAGCTTC 23
b      111442 AATATCTGGCCATTTCAGCTTC 111462

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RESULT 14				
AC125105/c				
LOCUS	277892 bp	DNA	linear	HTG 20-JUN-2002
DEFINITION	Mus musculus chromosome UNK clone RP24-220B7, WORKING DRAFT SEQUENCE, 60 unordered pieces.			
ACCESSION	AC125105			
VERSION	GI-21490578			
KEYWORDS	HTG; HTGS_PHASE1; SOURCE			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;			
REFERENCE	1 (bases 1 to 277892)			
AUTHORS	McPherson,J.D. and Waterston,R.H.			
TITLE	The sequence of Mus musculus clone			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 277892)			
AUTHORS	McPherson,J.D. and Waterston,R.H.			
TITLE	Direct Submission			
JOURNAL	Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park			
	St. Louis, MO 63108, USA			

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Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
Project Information
Genome project name: M BB0220B07
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location/Qualifiers
1. .191918
/organism="Mus musculus"
/db xref="taxon:10090"
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1. $.81\bar{0}$

911: .1960

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* 6550 6549: gap of unknown length
* 6551 7662: contig of 1013 bp in length
* 7663 7662: gap of unknown length
* 7664 9073: contig of 1311 bp in length
* 9074 9173: gap of unknown length
* 9174 10263: contig of 1090 bp in length
* 10264 10363: gap of unknown length
* 10364 11990: contig of 1627 bp in length
* 11991 12090: gap of unknown length
* 12091 13171: contig of 1081 bp in length
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* 13772 14786: contig of 1515 bp in length
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* 14887 16229: contig of 1343 bp in length
* 16230 16329: gap of unknown length
* 16330 18004: contig of 1675 bp in length
* 18005 18104: gap of unknown length
* 18106 19456: contig of 1352 bp in length
* 19457 19556: gap of unknown length
* 19557 21458: contig of 1902 bp in length
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* 21559 22675: contig of 1117 bp in length
* 22676 22775: gap of unknown length
* 22776 24272: contig of 1497 bp in length
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* 35109 35208: gap of unknown length
* 35209 36337: contig of 1428 bp in length
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* 38555 40244: contig of 1590 bp in length
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* 42636 44153: contig of 1518 bp in length
* 44154 44254 45967: contig of 1714 bp in length
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* 46068 47834 47933: contig of 1766 bp in length
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* 49440 52455: contig of 3016 bp in length
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* 55194 57493: contig of 2300 bp in length
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* 57594 59134 59233: contig of 1540 bp in length
* 59234 60952: contig of 1719 bp in length
* 60953 61952: gap of unknown length
* 61953 63195: contig of 2143 bp in length
* 63196 63295: gap of unknown length
* 63296 65553: contig of 2258 bp in length
* 65554 67988: gap of unknown length
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* 68089 71061: contig of 2973 bp in length
* 71062 71161: gap of unknown length

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* 71162 74202: contig of 3041 bp in length
* 74203 74302: gap of unknown length
* 74303 77181: contig of 2879 bp in length
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* 77282 80521: contig of 3240 bp in length
* 80522 80621: gap of unknown length
* 80622 83147: contig of 2526 bp in length
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* 83248 85358: contig of 2111 bp in length
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* 85459 89161: contig of 3703 bp in length
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* 89262 94379: contig of 5118 bp in length
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* 94480 97915: contig of 3436 bp in length
* 97916 98015: gap of unknown length
* 98016 103342: contig of 5327 bp in length
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* 103443 106304: contig of 2862 bp in length
* 106305 106404: gap of unknown length
* 111882: contig of 5478 bp in length
* 111883 111982: gap of unknown length
* 111983 116456: contig of 4474 bp in length
* 116457 116556: gap of unknown length
* 116557 122640: contig of 6084 bp in length
* 122641 122740: gap of unknown length
* 122741 133292: contig of 10552 bp in length
* 133293 133392: gap of unknown length
* 133393 144545: contig of 11153 bp in length
* 144546 144645: gap of unknown length
* 144646 160566: contig of 15921 bp in length
* 160567 160666: gap of unknown length
* 160667 181991: contig of 21325 bp in length
* 181992 182091: gap of unknown length
* 182092 216010: contig of 33919 bp in length
* 216011 216110: gap of unknown length
* 216111 276917: contig of 60807 bp in length
* 276918 277018 277892: contig of 875 bp in length.
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            /db_xref="taxon:10090"
            /chromosome="UNK"
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        1. .1214
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Query Match 84.3%; Score 19.4; DB 2; Length 277892;
 Best Local Similarity 95.2%; Pred. No. 1e+02;

Mon Apr 21 10:30:06 2003

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: April 18, 2003, 06:25:35
Job time : 582.273 secs

QY 3 AACTGGTGGCCATTTCAGCTTC 23
Db 132148 AAATGGTGGCCATTTCAGCTTC 132128

RESULT 15
BC013150/c
LOCUS BC013150 1520 bp mRNA linear PRI 29-AUG-2001
DEFINITION Homo sapiens, Similar to hypothetical protein FLJ22595, clone
MGC:17429 IMAGE:4340470, mRNA, complete cds.

ACCESSION BC013150
VERSION BC013150.1 GI:15341924
KEYWORDS MGC.

SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1520)

REFERENCE Strausberg,R.
AUTHORS Direct Submission
TITLE Submitted (27-AUG-2001) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 26 Row: 1 Column: 7.

FEATURES
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/clone="MGC:17429 IMAGE:4340470"
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/codon_start=1
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/translation="MGSVNSGHKAEQVVMGLDSAGKTTLLYKLKHQLVETLPTV
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BASE COUNT 414 a 372 c 431 g 303 t

ORIGIN

Query Match 81.7%; Score 18.8; DB 9; Length 1520;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTTCAGCTT 22

Db 226 CCAACTGGTGGCCCTTCAGCTT 205

GenCore version 5.1.4.p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:12:35 ; Search time 102.455 Seconds
(without alignments)
505.551 Million cell updates/sec

Title: US-09-270-437D-12

Perfect score: 23

Sequence: 1 ccaactgggtgcattcagcttc 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002:*

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6: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
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22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	AAZ36158	PCR primer for DNA
2	23	100.0	1708	AAZ36151	DNA encoding cance
3	23	100.0	1946	AAZ36153	An alternative for
4	18.8	81.7	415	AAK58003	Human immune/haema
5	18.8	81.7	1109	AAA49190	CDNA encoding huma
6	18.8	81.7	2568	ABL28587	Drosophila melanog
7	18.8	81.7	2834	ABL21504	Drosophila melanog
8	18.8	81.7	3722	AAK71737	Human immune/haema
9	18.8	81.7	4870	ABL28586	Drosophila melanog

C	10	17.8	77.4	3628	24	ABK63547	Rat sequence diffc
	11	17.8	77.4	8212	24	ABI99884	Mouse ischaemic co
	12	17.2	74.8	306	13	AAQ24805	Region 3' of human
	13	17.2	74.8	1019	18	AAV75063	Staphylococcus aur
	14	17.2	74.8	1203	13	AAQ24809	Mutant human D3 do
	15	17.2	74.8	1261	21	AAQ9614	Human D2 receptor
	16	17.2	74.8	1272	13	AAQ4803	Human D3 dopaminer
	17	17.2	74.8	1558	13	AAQ27988	Protease from S. A
	18	17.2	74.8	2325	16	AAQ24156	Enzyme Q36 coding
	19	17.2	74.8	3073	16	AAQ4158	Enzyme Q36 coding
C	20	17.2	74.8	4172	23	ABL12003	Drosophila melanog
	21	17.2	74.8	6781	23	ABL12002	Human immune/haema
	22	17.2	74.8	17170	22	AAK77880	Human immune/haema
	23	17.2	74.8	17173	22	AAK77881	Drosophila melanog
C	24	17.2	74.8	39159	23	ABL30024	Human genome-deriv
	25	16.8	73.0	258	24	ABS20709	Human genome-deriv
C	26	16.8	73.0	309	23	ABV61599	Human prostate exp
	27	16.8	73.0	454	24	ABS08292	Human prostate exp
C	28	16.8	73.0	7506	23	ABV24912	Human prostate exp
	29	16.6	72.2	510	22	AAK11576	Human brain expres
C	30	16.6	72.2	708	24	ABN67249	Streptococcus poly
	31	16.6	72.2	746	22	AAH99822	Human protein enco
C	32	16.6	72.2	1645	23	ABL09057	Drosophila melanog
	33	16.6	72.2	1987	23	ABL20943	Drosophila melanog
C	34	16.6	72.2	2224	20	AAZ10617	CDNA encoding a mu
	35	16.6	72.2	2305	23	ABV24225	Human prostate exp
C	36	16.6	72.2	2305	23	ABV24337	Human prostate exp
	37	16.6	72.2	2305	23	ABV24365	Human prostate exp
C	38	16.6	72.2	2379	23	ABL16853	Drosophila melanog
	39	16.6	72.2	2496	24	ABO67860	Listeria innocua D
C	40	16.6	72.2	2496	24	ABO69432	Listeria innocua D
	41	16.6	72.2	2575	24	ABQ70592	Listeria monocytog
C	42	16.6	72.2	2830	23	ABL17257	Drosophila melanog
	43	16.6	72.2	2971	23	ABL13725	Drosophila melanog
C	44	16.6	72.2	2980	23	ABL17175	Drosophila melanog
	45	16.6	72.2	4212	23	ABL12981	Drosophila melanog

ALIGNMENTS

```

RESULT 1
AAZ36158
ID  AAZ36158 standard; DNA; 23 Bp.
XX
AC  AAZ36158;
XX
DT  11-FEB-2000 (first entry)
XX
DE  PCR primer for DNA encoding cancer associated antigen KOC-2.
XX
KW  Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss.
XX
OS  Synthetic.
XX
OS  Homo sapiens.
XX
PN  WO954738-A1.
XX
PD  28-OCT-1999.
XX
PF  16-MAR-1999; 99WO-US05766.
XX
PR  17-APR-1998; 98US-0061709.
XX
XX  (LUDW-) LUDWIG INST CANCER RES.
XX  Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old L;
XX  WPI; 2000-013284/01.
XX  Nucleotides representing cancer-associated genes, used to develop
XX  products for the diagnosis, monitoring and treatment of cancers -

```

CC adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF).

XX SQ Sequence 1708 BP; 447 A; 469 C; 473 G; 314 T; 5 other;

Query Match 100.0%; Score 23; DB 21; Length 1708;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTTCAGCTTC 23
DB 68 CCAACTGGTGGCCATTTCAGCTTC 46

RESULT 3
AAZ36153/c
ID AAZ36153 standard; DNA; 1946 BP.

XX AC AAZ36153;

XX DT 11-FEB-2000 (first entry)

XX DE An alternative form of DNA encoding cancer associated antigen KOC-2.

XX KW Cancer associated antigen; KOC-2; cancer; vaccine; CT7; ss.

XX OS Homo sapiens.

XX PN WO9954738-A1.

XX PD 28-OCT-1999.

XX PF 16-MAR-1999; 99WO-US05766.

XX PR 17-APR-1998; 98US-0061709.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;

XX WPI; 2000-013284/01.

XX PT Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers

XX PS Claim 55; Page 42; 44pp; English.

XX CC The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 polynucleotide has some homology with MAGS-10, limited to about 210 amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of serine, proline, glutamine and leucine, and an almost invariable core of peptides which provoke lysis by cytolytic T cells. The polynucleotides and polypeptides can be used for screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF).

XX SQ Sequence 1946 BP; 502 A; 528 C; 553 G; 358 T; 5 other;

Query Match 100.0%; Score 23; DB 21; Length 1946;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTTCAGCTTC 23
DB 306 CCAACTGGTGGCCATTTCAGCTTC 284

PS Claim 108; Page 13; 44pp; English.

XX CC PCR primers AAZ36157-58 were used to amplify a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 polynucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of peptides which provoke lysis by cytolytic T cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF).

XX SQ Sequence 23 BP; 4 A; 8 C; 5 G; 6 T; 0 other;

Query Match 100.0%; Score 23; DB 21; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTTCAGCTTC 23

DB 1 CCAACTGGTGGCCATTTCAGCTTC 23

RESULT 2

AAZ36151/c

ID AAZ36151 standard; DNA; 1708 BP.

XX AC AAZ36151;

XX DT 11-FEB-2000 (first entry)

XX DE DNA encoding cancer associated antigen KOC-2.

XX KW Cancer associated antigen; KOC-2; cancer; vaccine; CT7; ss.

XX OS Homo sapiens.

XX PN WO9954738-A1.

XX PD 28-OCT-1999.

XX PF 16-MAR-1999; 99WO-US05766.

XX PR 17-APR-1998; 98US-0061709.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;

XX WPI; 2000-013284/01.

XX PT Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers

XX PS Claim 55; Page 40; 44pp; English.

XX CC The present sequence represents a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CT7. The CT7 polynucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of peptides which provoke lysis by cytolytic T cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an

RESULT 4
AAK58003/c
ID AAK58003 standard; CDNA; 415 BP.
AC AAK58003;
DT 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3063.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW Cytostatic; gene therapy; vaccine; metastasis; ss.
XX Homo sapiens.
XX WO200157182-A2.
FN 09-AUG-2001.
PD 17-JAN-2001; 2001WO-US01354.
PF 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
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PR 14-AUG-2000; 2000US-0225214.
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PR 14-AUG-2000; 2000US-0225270.
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PR 14-AUG-2000; 2000US-0225757.
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PR 18-AUG-2000; 2000US-0226279.
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PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
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PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
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PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237039.
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PR 01-NOV-2000; 2000US-0241826.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
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PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
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PR 08-NOV-2000; 2000US-0246610.
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PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
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PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX P-PSDB; AAM85222.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX Claim 1; SEQ ID NO 3063; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX SQ Sequence 415 BP; 92 A; 114 C; 130 G; 76 T; 3 other;
Query Match 81.7%; Score 18.8; DB 22; Length 415;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCAACTGGTGGCCATTTCAGCTT 22
Db 226 CCAGCTGGTGGCCCTTCAGCTT 205
RESULT 5
AAK49190/c
ID AAA49190 standard; cDNA; 1109 BP.
XX AC AAA49190;
XX DT 03-NOV-2000 (first entry)
XX DE cDNA encoding human GTPase associated protein-20.
XX KW Guanine nucleotide binding protein; GTP-binding protein; G-protein;
KW GTPase; GTPase associated protein; GTPAP; cell proliferation;
KW autoimmunity; inflammatory; immune system disorder; cancer; AIDS;
KW acquired immune deficiency syndrome; asthma; atherosclerosis;
KW arthritis; systemic lupus erythematosus; psoriasis; human; ss.
XX OS Homo sapiens.
XX FH Location/Qualifiers

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CDS 127..717
/*tag= a
/product= GTPAP20
FT FT
XX WO2000031263-A2.
PD 02-JUN-2000.
XX 23-NOV-1999; 99WO-US28013.
XX 23-NOV-1998; 98US-0109592.
PR 04-FEB-1999; 99US-0118610.
PR 06-APR-1999; 99US-0127990.
XX (INCY-) INCYTE PHARM INC.
XX Hillman JL, Tang YT, Bandman O, Lal P, Yue H, Lu DAM, Baughn MR;
PI Yang J, Azimzai Y;
XX WPI; 2000-400073/34.
DR P-PSDB; AAY99669.
XX Human GTPase associated proteins, polynucleotides, and antibodies,
PT useful for diagnosing, preventing and treating various diseases such as
PT atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS),
PT asthma, and autoimmune diseases -
XX Claim 9; Page 136; 144pp; English.
XX Human cDNA libraries from various tissues were screened for GTPase
CC associated proteins (GTPAP). The present sequence is cDNA encoding
CC human GTPAP-20. This sequence was derived from a cDNA library of the
CC wrist synovial membrane tissue from a female with rheumatoid arthritis.
CC This protein is expressed in reproductive, nervous and
CC gastrointestinal tissue. The GTPAP proteins may be used to define
CC agonists and antagonists of GTPAP activity and to generate antibodies
CC to GTPAP. This means the GTPAP proteins may be useful for treatment or
CC prevention of diseases associated with GTPAP such as cell proliferation
CC disorders, autoimmune disorders, inflammatory disorders, immune system
CC disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic
CC lupus erythematosus and psoriasis.
XX SQ Sequence 1109 BP; 264 A; 297 C; 334 G; 214 T; 0 other;
Query Match 81.7%; Score 18.8; DB 21; Length 1109;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCAACTGGTGGCCATTTCAGCTT 22
Db 238 CCAGCTGGTGGCCCTTCAGCTT 217
RESULT 6
ABL28587/c
ID ABL28587 standard; DNA; 2568 BP.
XX AC ABL28587;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37234.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX OS Drosophila melanogaster.
XX PN WO2000171042-A2.
XX PD 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.

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XX PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Claim 1; SEQ ID NO 37234; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 2568 BP; 686 A; 575 C; 664 G; 643 T; 0 other;
 CC Query Match 81.7%; Score 18.8; DB 23; Length 2568;
 CC Best Local Similarity 90.9%; Pred. No. 37;
 CC Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAACGTGGTGCCTCAGCTTC 23
 DB 1965 CAACGTGGTGCCTCAGCTTC 1944
 RESULT 7
 ABL21504
 ID ABL21504 standard; DNA; 2834 BP.
 XX AC ABL21504;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15985.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical; gene; ds.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Claim 1; SEQ ID NO 37234; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 2568 BP; 686 A; 575 C; 664 G; 643 T; 0 other;
 CC Query Match 81.7%; Score 18.8; DB 23; Length 2568;
 CC Best Local Similarity 90.9%; Pred. No. 37;
 CC Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAACGTGGTGCCTCAGCTTC 23
 DB 1965 CAACGTGGTGCCTCAGCTTC 1944

PS Claim 1; SEQ ID NO 15985; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 2834 BP; 747 A; 689 C; 625 G; 773 T; 0 other;
 CC Query Match 81.7%; Score 18.8; DB 23; Length 2834;
 CC Best Local Similarity 90.9%; Pred. No. 37;
 CC Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAACGTGGTGCCTCAGCTTC 23
 DB 2773 CAACGTGGTGCCTCAGCTTC 2794
 RESULT 8
 AAK71737/c
 ID AAK71737 standard; DNA; 3722 BP.
 XX AC AAK71737;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26549.
 XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX OS Homo sapiens.
 XX PN WO200157182-A2.
 XX PD 09-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US01354.
 XX PR 31-JAN-2000; 2000US-0179065.
 XX PR 04-FEB-2000; 2000US-0180628.
 XX PR 24-FEB-2000; 2000US-0184664.
 XX PR 02-MAR-2000; 2000US-0186350.
 XX PR 16-MAR-2000; 2000US-0189874.
 XX PR 17-MAR-2000; 2000US-0190076.
 XX PR 18-APR-2000; 2000US-0198123.
 XX PR 19-MAY-2000; 2000US-0205515.
 XX PR 07-JUN-2000; 2000US-0209467.
 XX PR 28-JUN-2000; 2000US-0214886.
 XX PR 30-JUN-2000; 2000US-0215135.
 XX PR 07-JUL-2000; 2000US-0216647.
 XX PR 07-JUL-2000; 2000US-0216880.
 XX PR 11-JUL-2000; 2000US-0217487.
 XX PR 11-JUL-2000; 2000US-0217496.
 XX PR 14-JUL-2000; 2000US-0218290.
 XX PR 26-JUL-2000; 2000US-0220963.
 XX PR 26-JUL-2000; 2000US-0220964.
 XX PR 14-AUG-2000; 2000US-0224518.
 XX PR 14-AUG-2000; 2000US-0224519.
 XX PR 14-AUG-2000; 2000US-0225213.
 XX PR 14-AUG-2000; 2000US-0225214.
 XX PR 14-AUG-2000; 2000US-0225266.
 XX PR 14-AUG-2000; 2000US-0225267.
 XX PR 14-AUG-2000; 2000US-0225268.
 XX PR 14-AUG-2000; 2000US-0225270.
 XX PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246529.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 26549; 307lpp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX Sequence 3722 BP; 990 A; 887 C; 926 G; 919 T; 0 other;
XX
XX Query Match 81.7%; Score 18.8; DB 22; Length 3722;
XX Best Local Similarity 90.9%; Pred. NO. 39;
XX Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTCAGCTT 22
 Db 2041 CCAGCTGGTGGCCCTTCAGCTT 2020

RESULT 9

ABL28586
 ID ABL28586 standard; DNA; 4870 BP.
 AC ABL28586;
 XX XX

DT 26-MAR-2002 (first entry)
 XX XX

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37231.
 XX XX

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 XX XX

OS Drosophila melanogaster.
 XX XX

PN WO200171042-A2.
 XX XX

PD 27-SEP-2001.
 XX XX

XX 23-MAR-2001; 2001WO-US09231.
 XX XX

PR 23-MAR-2000; 2000US-191637P.
 PR XX

XX 11-JUL-2000; 2000US-0614150.
 XX XX

PA (PEXE) PE CORP NY.
 XX XX

XX Venter JC, Adams M, Li PWD, Myers EW;
 PI XX

XX WPI; 2001-656860/75.
 DR XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX XX

PS Claim 1; SEQ ID NO 37231; 21pp + Sequence Listing; English.
 XX XX

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (AB057737-AB072072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX XX

SQ Sequence 4870 BP; 1239 A; 1201 C; 1083 G; 1347 T; 0 other;
 Query Match 81.7%; Score 18.8; DB 23; Length 4870;
 Best Local Similarity 90.9%; Pred. No. 41;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAACTGGTGGCCATTCAGCTTC 23
 Db 1662 CCAACTGGTGGCCATTCAGCTTC 1683

RESULT 10

ABK63547/c
 ID ABK63547 standard; cDNA; 3628 BP.
 AC ABK63547;
 XX XX

DT 18-JUN-2002 (first entry)
 XX XX

DE Rat sequence differentially expressed in response to a hepatotoxin #1454.
 XX XX

XX XX

KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 KW differential expression; centrilobular necrosis; steatosis.
 XX XX

OS Rattus norvegicus.
 XX XX

PN WO200210453-A2.
 XX XX

PD 07-FEB-2002.
 XX XX

PF 30-JUL-2001; 2001WO-US23872.
 XX XX

PR 31-JUL-2000; 2000US-222040P.
 PR XX

PR 02-NOV-2000; 2000US-244880P.
 PR XX

PR 11-MAY-2001; 2001US-290029P.
 PR XX

PR 15-MAY-2001; 2001US-290645P.
 PR XX

PR 22-MAY-2001; 2001US-292336P.
 PR XX

PR 06-JUN-2001; 2001US-295798P.
 PR XX

PR 13-JUN-2001; 2001US-297457P.
 PR XX

PR 19-JUN-2001; 2001US-298884P.
 PR XX

PR 09-JUL-2001; 2001US-303459P.
 XX XX

PA (GENE-) GENE LOGIC INC.
 XX XX

XX Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 PI XX

XX WPI; 2002-241625/29.
 XX XX

XX Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells -
 XX XX

PS Claim 1; Seq ID No 1454; 239pp; English.
 XX XX

XX The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression.
 CC The method can also be used to identify an agent which modulates the
 CC toxic response and predict cellular pathways that a compound modulates
 CC in a cell. The methods utilise a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information,
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.
 XX XX

SQ Sequence 3628 BP; 1035 A; 698 C; 838 G; 1057 T; 0 other;
 Query Match 77.4%; Score 17.8; DB 24; Length 3628;
 Best Local Similarity 90.5%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACTGGTGGCCATTCAGCTTC 23

```

XX DE Region 3' of human D3 dopaminergic receptor ORF.
XX KW G-protein-coupled receptors; tumour; psychosis; Parkinson's disease;
XX KW arterial hypertension; hypothalamo-hypophyseal axis;
XX KW open reading frame; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT misc_feature 47..240
XX FT /*tag= a
XX FT /note= "corresponds to nucleotides
XX FT 1013-1206 of AAQ24803"
XX PN WO9207937-A.
XX PD 14-MAY-1992.
XX PF 16-OCT-1991; 91WO-FR00810.
XX PR 06-NOV-1990; 90FR-0013731.
XX PA (INRM ) INSERM INST NAT SANTE RECH MEDICALE.
XX PI Giros B, Martres MP, Schwartz JC, Sokoloff P;
XX WIPI; 1992-183673/22.
XX PT Human D3 dopaminergic receptor polypeptide(s) - for in-vitro
XX PT screening of new dopaminergic drugs and diagnosis and treatment
XX PT of various psychiatric, cardiovascular, neurological and
XX PT neuro-endocrinological disorders
XX PS Claim 4; Fig 4; Slipp; French.
XX CC A Sau3A human genomic DNA bank was screened with two rat D3 receptor
XX CC probes to identify open reading frames. The rat D3 probe #2
XX CC containing the coding sequence for the C-terminal part and
XX CC transmembrane domains VI and VII of rat D3 identified 1 positive
XX CC clone. The sequence given here corresponds to part of the 3'
XX CC region of the human D3 gene. This sequence is one of the preferred
XX CC fragments able to code for a polypeptide with the properties of
XX CC the human D3 receptor. The sequence is also useful as a probe to
XX CC diagnose e.g. pathological expression of the D3 receptor,
XX CC polymorphism of the D3 receptor gene or point mutations.
XX CC See AAQ24803-9.
XX SQ Sequence 306 BP; 63 A; 92 C; 69 G; 82 T; 0 other;
XX Query Match 74.8%; Score 17.2; DB 13; Length 306;
XX Best Local Similarity 86.4%; Pred. No. 1.5e+02;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGAGCTT 22
    |||||
Db 4 CCAATGGTGGCCATTGCTT 25
    |||||

RESULT 13
AAV75063
ID AAV75063 standard; DNA; 1019 BP.
XX AC AAV75063;
XX DT 16-MAR-1999 (first entry)
XX DE Staphylococcus aureus contig SEQ ID #752.
XX KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
XX KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX KW skin infection; surgical wound infection; scalded skin syndrome;
XX KW toxic shock syndrome; ds.

Db 1355 AGCTGGAGGCCATTGAGCTTC 1335
|||||
RESULT 11
ABI99884
ID ABI99884 standard; cDNA; 8212 BP.
XX AC ABI99884;
XX DT 07-MAR-2002 (first entry)
XX DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:1027.
XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX OS Mus musculus.
XX PN WO200188188-A2.
XX PD 22-NOV-2001.
XX PF 18-MAY-2001; 2001WO-JP04192.
XX PR 18-MAY-2000; 2000JP-0145977.
XX PA (UINI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX WIPI; 2002-034733/04.
XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
XX PT expression levels of particular genes defined in the specification or
XX PT by determining the expression profile of a gene group comprising these
XX PT genes -
XX PS Claim 2; Page 2592-2596; 2690pp; English.
XX CC The present invention describes a method for examining ischemic
XX CC conditions, comprising measuring the expression levels of particular
XX CC genes (1) in a test sample or determining the expression profile of a
XX CC gene group in the sample comprising genes selected from (I). The method
XX CC is useful for examining the ischemic condition (e.g. compressive
XX CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
XX CC expression levels of particular genes (ABI99202 to ABI99912, encoding
XX CC the protein sequences in ABB57020 to ABB57374) or by determining the
XX CC expression profile of a gene group comprising these genes. The
XX CC expression levels or expression profiles produced by these genes are
XX CC used as an indicator when screening for ischaemic condition-improving
XX CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
XX CC represent PCR primers for a mouse ischaemic condition related sequence,
XX CC which are used in the exemplification of the present invention.
XX SQ Sequence 8212 BP; 1663 A; 2301 C; 2300 G; 1948 T; 0 other;
XX Query Match 77.4%; Score 17.8; DB 24; Length 8212;
XX Best Local Similarity 90.5%; Pred. No. 1.3e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AACCTGGTGCCATTGAGCTTC 23
    |||||
Db 1006 AACCTGGTGCCATTGAGCTTC 1026
    |||||

RESULT 12
AAQ24805
ID AAQ24805 standard; DNA; 306 BP.
XX AC AAQ24805;
XX DT 19-NOV-1992 (first entry)
```

XX OS Staphylococcus aureus.

XX FH Key Location/Qualifiers

XX FT misc_feature 901..960

XX FT /*tag= a

XX FT /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

XX FT

XX FT

XX PN EP786519-A2.

XX XX

XX PD 30-JUL-1997.

XX XX

XX PF 07-JAN-1997; 97EP-0100117.

XX XX

XX PR 05-JAN-1996; 96US-0009861.

XX XX

XX PA (HUMA-) HUMAN GENOME SCI INC..

XX PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;

XX PI Rosen CA;

XX XX

XX DR WPI; 1997-374922/35.

XX XX

XX PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -

XX PT stored on computer readable medium and used in the production of

XX PT anti-S.aureus vaccines

XX XX

XX PS Claim 1; Page 1646-1647; 3271pp; English.

XX CC

XX CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.

XX SQ

XX SQ Sequence 1019 BP; 364 A; 194 C; 159 G; 240 T; 62 other;

XX

XX Query Match 74.8%; Score 17.2; DB 18; Length 1019;

XX Best Local Similarity 86.4%; Pred. No. 1.8e+02;

XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX

XX QY 2 CAACCTGGTGGCCATTGCTTC 23

XX DB 640 CAACCTGGTGGTAAATTCAGGTT 661

XX

XX RESULT 14

XX AAQ24809

XX ID AAQ24809 standard; DNA; 1203 BP.

XX XX

XX AC AAQ24809;

XX XX

XX DT 19-NOV-1992 (first entry)

XX DE Mutant human D3 dopaminergic receptor.

XX XX

XX KW G-protein-coupled receptors; tumour; psychosis; Parkinson's disease;

KW arterial hypertension; hypothalamo-hypophyseal axis; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT mutation 25

XX FT /*tag= a

XX FT /note= "A is replaced by G"

XX FT mutation 51

XX FT /*tag= b

XX FT /note= "A is replaced by G"

XX FT mutation 236

XX FT /*tag= c

XX FT /note= "C is replaced by T"

XX FT mutation 565

XX FT /*tag= d

XX FT /note= "G is replaced by A"

XX FT mutation 876

XX FT /*tag= e

XX FT /note= "T is replaced by C"

XX FT mutation 1190

XX FT /*tag= f

XX FT /note= "T is replaced by C"

XX XX

XX PN WO9207937-A.

XX XX

XX PD 14-MAY-1992.

XX XX

XX PF 16-OCT-1991; 91WO-FR00810.

XX XX

XX PR 06-NOV-1990; 90FR-0013731.

XX XX

XX PA (INRM) INERM INST NAT SANTE RECH MEDICALE.

XX XX

XX PI Giros B, Martres MP, Schwartz JC, Sokoloff P;

XX XX

XX DR WPI; 1992-183673/22.

XX DR P-PSDB; AAR24247.

XX XX

XX PT Human D3 dopaminergic receptor polypeptide(s) - for in-vitro screening of new dopaminergic drugs and diagnosis and treatment of various psychiatric, cardiovascular, neurological and neuro-endocrinological disorders

XX XX

XX PS Claim 4; Page 37; 51pp; French.

XX CC

XX CC This ORF codes for a mutant D3 receptor with four amino acid substitutions relative to the wild-type receptor sequence (two of the nucleotide substitutions are silent). The mutant receptor retains its dopaminergic receptor properties. The mutant containing all the mutations in the Features Table is preferred but mutants which contain at least one of the mutations are also covered by the invention. See AAQ24803-8.

XX SQ

XX SQ Sequence 1203 BP; 252 A; 351 C; 311 G; 289 T; 0 other;

XX

XX Query Match 74.8%; Score 17.2; DB 13; Length 1203;

XX Best Local Similarity 86.4%; Pred. No. 1.9e+02;

XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX

XX QY 1 CCAACTGGTGCCATTGCTT 22

XX DB 984 CCAATGGTGCCATTGCTT 1005

XX

XX RESULT 15

XX AAA99614

XX ID AAA99614 standard; cDNA; 1261 BP.

XX XX

XX AC AAA99614;

XX XX

XX DT 02-FEB-2001 (first entry)

XX XX

us-09-270-437d-12.rng

Mon Apr 21 10:30:08 2003

```

DE Human D2 receptor cDNA.
XX Human; D4 dopamine receptor; cardiovascular system; retinal tissue;
KW vasoregulator; D2 receptor; ss.
XX Homo sapiens.
OS
XX US6121015-A.
PN
XX 19-SEP-2000.
PD
XX 07-JUN-1995; 95US-0475742.
PF
XX 16-JUN-1994; 94US-0261293.
PR 28-JAN-1993; 93US-0014013.
PT
XX (UNIW ) UNIV WASHINGTON.
PA
XX Todd RD, O'Malley KL;
PI
XX WPI; 2000-655527/63.
DR
XX Screening for compounds that selectively bind to a rat D4 dopamine
PT receptor (DDR), useful for identifying dopamine (ant)agonists.
PT comprises exposing cells transfected with a nucleic acid encoding the
PT DDR to candidate compounds -
XX
XX Example 2; Column 35-38; 29pp; English.
PS
XX The present sequence is the human D2 receptor cDNA. The sequence was
CC expressed in the same cell line as the putative rat D4 receptor gene in
CC a method to confirm that the putative D4 receptor does code for a
CC dopamine receptor analogous to the human D4 receptor. The rat D4 receptor
CC was shown to preferentially bind dopamine antagonists such as clozapine.
CC The D4 receptor cDNA is useful for screening drugs which specifically
CC bind to the receptor and have selective effects on the cardiovascular
CC and retinal tissues through interactions with the receptor. Such
CC compounds may act as vasoregulators or may have ionotropic effects. The
CC D4 receptor protein may be used for the production of polyclonal or
CC monoclonal antibodies which recognise the D4 receptor sequence but do not
CC recognise other dopaminergic receptors. The antibodies may be used in
CC immunocytochemical studies and for identification and isolation via flow
CC sorting of D4 expressing cell types.
XX
XX Sequence 1261 BP; 265 A; 363 C; 328 G; 305 T; 0 other;
SQ
Query Match 74.8%; Score 17.2; DB 21; Length 1261;
Best Local Similarity 86.4%; Pred. NO. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCAACTGGTGGCCATTGCGTT 22
Db 990 CCAATGGTGGCCATTGCGTT 1011

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Search completed: April 18, 2003, 05:45:26
Job time : 105.455 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:53:41 ; Search time 22.4773 Seconds
(without alignments)
313.809 Million cell updates/sec

Title: US-09-270-437D-12

Perfect score: 23
Sequence: 1 ccaactggtggccattcagcttc 23

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338361 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCTUS COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	23	100.0	1708	4	US-09-061-709-5
C 2	23	100.0	1946	4	US-09-061-709-7
C 3	17.2	74.8	1261	3	US-08-475-742-16
C 4	17.2	74.8	2325	2	US-08-714-677-3
C 5	17.2	74.8	2325	2	US-08-393-540-3
C 6	17.2	74.8	2325	2	US-08-714-537-3
C 7	17.2	74.8	3073	2	US-08-714-677-11
C 8	17.2	74.8	3073	2	US-08-393-540-11
C 9	17.2	74.8	3073	2	US-08-714-537-11
C 10	16.6	72.2	2224	4	US-09-261-855-1
C 11	16.2	70.4	112	1	US-08-518-878B-29
C 12	16.2	70.4	112	1	US-08-518-878B-30
C 13	16.2	70.4	112	1	US-08-294-522B-29
C 14	16.2	70.4	112	1	US-08-294-522B-30
C 15	16.2	70.4	112	2	US-08-807-861A-29
C 16	16.2	70.4	112	2	US-08-807-861A-30
C 17	16.2	70.4	112	2	US-08-470-868A-29
C 18	16.2	70.4	112	2	US-08-470-868A-30
C 19	16.2	70.4	112	3	US-09-210-681-29
C 20	16.2	70.4	112	3	US-09-210-681-30
C 21	16.2	70.4	112	3	US-08-946-719A-29
C 22	16.2	70.4	112	3	US-08-946-719A-30
C 23	16.2	70.4	3941	4	US-09-408-865-2
C 24	16	69.6	1445	1	US-08-324-533-1
C 25	15.8	68.7	1238	4	US-09-313-300-10
C 26	15.8	68.7	1434	4	US-09-129-112-18
C 27	15.6	67.8	401	4	US-09-323-873A-12

28	15.6	67.8	453	2	US-08-419-075-5	Sequence 5, Appli
C 29	15.6	67.8	1038	4	US-09-004-838-128	Sequence 128, App
C 30	15.6	67.8	1177	3	US-08-611-587-7	Sequence 7, Appli
C 31	15.6	67.8	1644	2	US-08-458-555-1	Sequence 1, Appli
C 32	15.6	67.8	1719	4	US-09-149-476-152	Sequence 152, App
C 33	15.6	67.8	2277	1	US-08-676-967-5	Sequence 5, Appli
C 34	15.6	67.8	2277	1	US-08-676-974-5	Sequence 5, Appli
C 35	15.6	67.8	2277	2	US-09-098-487-5	Sequence 5, Appli
C 36	15.6	67.8	2299	2	US-09-293-549-13	Sequence 5, Appli
C 37	15.6	67.8	2316	2	US-08-714-677-1	Sequence 13, Appli
C 38	15.6	67.8	2316	2	US-08-393-540-1	Sequence 1, Appli
C 39	15.6	67.8	2316	2	US-08-714-537-1	Sequence 1, Appli
C 40	15.6	67.8	2738	2	US-08-795-868-17	Sequence 17, Appl
C 41	15.6	67.8	2738	4	US-09-303-069-17	Sequence 17, Appl
C 42	15.6	67.8	2738	4	US-09-134-250-17	Sequence 17, Appl
C 43	15.6	67.8	2936	2	US-08-714-677-10	Sequence 10, Appl
C 44	15.6	67.8	2936	2	US-08-393-540-10	Sequence 10, Appl
C 45	15.6	67.8	2936	2	US-08-714-537-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-061-709-5/c
; Sequence 5, Application US/09061709B
; Patent No. 6297364
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseung
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/061,709B
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 5
; LENGTH: 1708
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-061-709-5

Query Match 100.0%; Score 23; DB 4; Length 1708;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 68 CCAACTGGTGGCCATTGAGCTTC 46

RESULT 2

US-09-061-709-7/c
; Sequence 7, Application US/09061709B
; Patent No. 6297364
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseung
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/061,709B

us-09-270-437d-12.rni

Mon Apr 21 10:30:09 2003

STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,677
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,540
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: JP 090728
FILING DATE: 06-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047956
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047940
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 090705
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUBOTA=4
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2325
US-08-714-677-3

Query Match 100.0%; Score 23; DB 4; Length 1946;
Best Local Similarity 100.0%; Pred. No. 0.044; 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

Qy 1 CCACTGGTGGCCATTGAGCTTC 23
Db 306 CCACTGGTGGCCATTGAGCTTC 284

RESULT 3
US-08-475-742-16
Sequence 16, Application US/08475742
Patent No. 6121015
GENERAL INFORMATION:
APPLICANT: O'Malley, Karen L
APPLICANT: Todd, Richard D
TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
FILE REFERENCE: WU 102 CON DIV
CURRENT APPLICATION NUMBER: US/08/475,742
CURRENT FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: US 08/261,293
EARLIER FILING DATE: 1994-06-16
EARLIER APPLICATION NUMBER: US 08/014,013
EARLIER FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 1261
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1261)
OTHER INFORMATION: Human d3 cDNA
PUBLICATION INFORMATION:
JOURNAL: C. R. Acad. Sci., D, Sci. Nat.
VOLUME: 311
PAGES: 501-508
DATE: 1990
US-08-475-742-16

Query Match 74.8%; Score 17.2; DB 3; Length 1261;
Best Local Similarity 86.4%; Pred. No. 24; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3;

Qy 1 CCACTGGTGGCCATTGAGCTT 22
Db 990 CCAATGGTGGCCATTGCTT 1011

RESULT 4
US-08-714-677-3
Sequence 3, Application US/08714677
Patent No. 5871977
GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: MARUTA, Kazuhiko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.

Query Match 74.8%; Score 17.2; DB 2; Length 2325;
Best Local Similarity 86.4%; Pred. No. 26; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3;

Qy 2 CCACTGGTGGCCATTGAGCTTC 23
Db 1896 CAACGGGGCCGCTTCAGCTTC 1917

RESULT 5
US-08-393-540-3
Sequence 3, Application US/08393540
Patent No. 5871993
GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: MARUTA, Kazuhiko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.

Query Match 74.8%; Score 17.2; DB 3; Length 1261;
Best Local Similarity 86.4%; Pred. No. 24; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3;

Qy 1 CCACTGGTGGCCATTGAGCTT 22
Db 990 CCAATGGTGGCCATTGCTT 1011

RESULT 4
US-08-714-677-3
Sequence 3, Application US/08714677
Patent No. 5871977
GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: MARUTA, Kazuhiko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.

Query Match 74.8%; Score 17.2; DB 3; Length 1261;
Best Local Similarity 86.4%; Pred. No. 24; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3;

Qy 1 CCACTGGTGGCCATTGAGCTT 22
Db 990 CCAATGGTGGCCATTGCTT 1011

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,540
FILING DATE: 23-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 090728
FILING DATE: 06-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047956
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047940
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 090705
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUBOTA=4
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2325
US-08-393-540-3

Query Match 74.8%; Score 17.2; DB 2; Length 2325;
Best Local Similarity 86.4%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAACGTGGTGGCCATTACGCTTC 23
|||||
DB 1896 CAACCGCGCGCGTTCAGCTTC 1917

RESULT 6
US-08-714-537-3
Sequence 3, Application US/08714537
Patent No. 5871994
GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: MARUTA, Kazuhiko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,540
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: JP 090728
FILING DATE: 06-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047956
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047940
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 090705
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUBOTA=4
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2325
US-08-714-537-3

Query Match 74.8%; Score 17.2; DB 2; Length 2325;
Best Local Similarity 86.4%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAACGTGGTGGCCATTACGCTTC 23
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DB 1896 CAACCGCGCGCGTTCAGCTTC 1917

RESULT 7
US-08-714-677-11
Sequence 11, Application US/08714677
Patent No. 5871977
GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: MARUTA, Kazuhiko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 090728
FILING DATE: 06-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047956
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047940
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 090705
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUBOTA-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3073 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 678..3002
US-08-393-540-11

Query Match 74.8%; Score 17.2; DB 2; Length 3073;
Best Local Similarity 86.4%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAACTGGTGGCCATTCAGCTTC 23
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DB 2573 CAACGGCGCGCGTTCAGCTTC 2594

RESULT 9
US-08-714-537-11
Sequence 11, Application US/08714537
Patent No. 5871994
GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Kenji
APPLICANT: MARUTA, Kazuhiko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/714,537
APPLICATION NUMBER: US/08/714,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,540
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: JP 090728
FILING DATE: 06-APR-1994

APPLICATION NUMBER: US/08/714,677
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/393,540
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: JP 090728
FILING DATE: 06-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047956
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 047940
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 090705
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUBOTA=4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3073 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 678..3002

US-08-714-677-11

Query Match 74.8%; Score 17.2; DB 2; Length 3073;
Best Local Similarity 86.4%; Pred No. 27;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAACTGGTGGCCATTCAGTTC 23
||||| ||||| ||||| |||||
Db 2573 CAACGGGCGCGTTCAGTTC 2594

RESULT 8
US-08-393-540-11
; Sequence 11, Application US/08393540
; Patent No. 5871993
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Kenji
; APPLICANT: MARUTA, Kazuhiko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,540
; FILING DATE: 23-FEB-1995
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 047956
;; FILING DATE: 23-FEB-1994
;; PRIOR APPLICATION DATA: JP 047940
;; FILING DATE: 23-FEB-1994
;; PRIOR APPLICATION DATA: JP 090705
;; FILING DATE: 06-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: KUBOTA-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3073 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 678..3002
US-08-714-537-11

Query Match 74.8%; Score 17.2; DB 2; Length 3073;
Best Local Similarity 86.4%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAACTGGTGGCCATTCAGCTTC 23
DB 2573 CAACCGGGCGCGCTTCAGCTTC 2594

RESULT 10

US-09-261-855-1/c
; Sequence 1, Application US/09261855A
; Patent No. 625055
; GENERAL INFORMATION:
; APPLICANT: Rose, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/261,855A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 1
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-261-855-1

Query Match 72.2%; Score 16.6; DB 4; Length 2224;
Best Local Similarity 82.6%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTCAGCTTC 23
DB 563 CCAGTTGATGGCCATTAGCTTC 541

RESULT 11

US-08-518-8788-29/c
; Sequence 29, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/518,878B
;; FILING DATE: 23-AUG-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-036
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 112 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-518-878B-29

Query Match 70.4%; Score 16.2; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AACTGGTGGCCATTCAGCTTC 23
DB 62 ACCTGAGGGCATTAGCTTC 42

RESULT 12

US-08-518-878B-30/c
; Sequence 30, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,878B
; FILING DATE: 23-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090

us-09-270-437d-12.rni

Mon Apr 21 10:30:09 2003

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; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-518-878B-30

Query Match 70.4%; Score 16.2; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AACTGGTGGCCATTCAGCTTC 23
Db 62 AGCTGGAGGCGATTCAGCTTC 42

RESULT 13
US-08-294-522B-29/c
; Sequence 29, Application US/08294522B
; Patent No. 5741666
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: Compositions and Methods for the
; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 48
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,522B
; FILING DATE: 23-AUG-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-294-522B-30

Query Match 70.4%; Score 16.2; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AACTGGTGGCCATTCAGCTTC 23
Db 62 AGCTGGAGGCGATTCAGCTTC 42

RESULT 14
US-08-294-522B-30/c
; Sequence 30, Application US/08294522B

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; Patent No. 5741666
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: Compositions and Methods for the
; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,522B
; FILING DATE: 23-AUG-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-294-522B-30

Query Match 70.4%; Score 16.2; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AACTGGTGGCCATTCAGCTTC 23
Db 62 AGCTGGAGGCGATTCAGCTTC 42

RESULT 15
US-08-807-861A-29/c
; Sequence 29, Application US/08807861A
; Patent No. 5853975
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,861A
; FILING DATE: 26-FEB-1997
; CLASSIFICATION: 514

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/518,878
; FILING DATE: 23-AUG-1995
; APPLICATION NUMBER: US 08/470,868
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/294,522
; FILING DATE: 23-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-807-861A-29

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Query Match          70.4%; Score 16.2; DB 2; Length 112;
Best Local Similarity 85.7%; Pred No. 50;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 3 AACTGGTGGCCATTTCAGCTTC 23
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Db 62 AGCTGGAGGGCATTTCAGCTTC 42

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Job time : 23.4773 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:31 ; Search time 95.4848 Seconds
(without alignments)
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Title: US-09-270-437D-12

Perfect score: 23
Sequence: 1 ccaactgggtgcccattcagcttc 23

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Searched: 639749 seqs, 502280978 residues

Total number of hits satisfying chosen parameters: 1279498

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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 - 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
 - 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 - 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23	100.0	1708	10	US-09-899-651-5
C 2	23	100.0	1946	10	US-09-899-651-7
C 3	17.8	77.4	3628	10	US-09-917-800A-1454
C 4	17.2	74.8	1019	7	US-08-781-986A-752
C 5	16.8	73.0	258	10	US-09-864-761-32265
C 6	16.8	73.0	454	10	US-09-864-761-15758
C 7	16.6	72.2	453	10	US-09-960-352-11802
C 8	16.6	72.2	510	10	US-09-864-761-13431
C 9	16.6	72.2	2224	10	US-09-873-637-1
C 10	16.2	70.4	709	10	US-09-864-761-21356
C 11	16.2	70.4	1632	9	US-09-938-842A-1201
C 12	16.2	70.4	1994	10	US-09-864-761-4614
C 13	16.2	70.4	2244	9	US-09-372-348-14
C 14	16.2	70.4	2418	9	US-09-938-842A-1478
C 15	16.2	70.4	8001	9	US-10-261-482-3
C 16	16.2	70.4	536165	9	US-09-939-964-1
C 17	16	69.6	822	10	US-09-893-737-293
C 18	15.8	68.7	553	10	US-09-864-761-7260
C 19	15.8	68.7	1356	10	US-09-815-242-6624

C 20	15.8	68.7	1434	10	US-09-129-112-18
C 21	15.8	68.7	1506	10	US-09-822-830A-124
C 22	15.8	68.7	3939	9	US-10-006-856A-226
C 23	15.8	68.7	3939	9	US-10-006-818A-226
C 24	15.8	68.7	3939	9	US-10-015-393A-226
C 25	15.8	68.7	11597	10	US-09-070-927A-222
C 26	15.6	67.8	130	10	US-09-864-761-25655
C 27	15.6	67.8	157	10	US-09-864-761-24471
C 28	15.6	67.8	171	10	US-09-864-761-21232
C 29	15.6	67.8	189	10	US-09-864-761-28773
C 30	15.6	67.8	256	10	US-09-867-550-2059
C 31	15.6	67.8	401	9	US-10-011-095-12
C 32	15.6	67.8	401	9	US-10-010-667A-12
C 33	15.6	67.8	447	10	US-09-864-761-4484
C 34	15.6	67.8	450	10	US-09-864-761-6525
C 35	15.6	67.8	455	10	US-09-924-035A-218
C 36	15.6	67.8	457	10	US-09-770-444-511
C 37	15.6	67.8	509	10	US-09-864-761-8998
C 38	15.6	67.8	579	10	US-09-864-761-7767
C 39	15.6	67.8	595	10	US-09-864-761-12193
C 40	15.6	67.8	626	10	US-09-920-300A-69
C 41	15.6	67.8	626	12	US-10-033-528-69
C 42	15.6	67.8	1038	10	US-09-789-561-17
C 43	15.6	67.8	1169	10	US-09-747-835A-11
C 44	15.6	67.8	1209	9	US-10-098-841-86
C 45	15.6	67.8	1341	10	US-09-954-456-509

ALIGNMENTS

RESULT 1
US-09-899-651-5/c
; Sequence 5, Application US/09899651
; Patent No. US20020111470A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 538
; CURRENT APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 5
; LENGTH: 1708
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-5

Query Match 100.0%; Score 23; DB 10; Length 1708;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGCTTC 23
Db 68 CCAACTGGTGGCCATTGCTTC 46

RESULT 2
US-09-899-651-7/c
; Sequence 7, Application US/09899651
; Patent No. US20020111470A1
; GENERAL INFORMATION:

Mon Apr 21 10:30:11 2003

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US-09-917-800A-1454
Query Match      77.4%; Score 17.8; DB 10; Length 3628;
Best Local Similarity 90.5%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACTGGTGGCCATTACGCTTC 23
DB 1355 AGCTGGAGGCCATTACGCTTC 1335

RESULT 4
US-08-781-986A-752
; Sequence 752, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781.986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 752:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-752

Query Match      74.8%; Score 17.2; DB 7; Length 1019;
Best Local Similarity 86.4%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAACTGGTGGCCATTACGCTTC 23
DB 640 CAACTGGTGGTAATTCAGCTTC 661

RESULT 5
US-09-864-761-32265/c
; Sequence 32265, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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US-09-917-800A-1454/c
; Sequence 1454, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1454
; LENGTH: 3628
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 U20796

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Query Match      100.0%; Score 23; DB 10; Length 1946;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCAACTGGTGGCCATTACGCTTC 23
DB 306 CCAACTGGTGGCCATTACGCTTC 284

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; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32265
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002093.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.5
; OTHER INFORMATION: EST HUMAN HIT: BE798126.1, EVALUE 1.00e-114
; OTHER INFORMATION: SWISSPROT HIT: P34369, EVALUE 8.00e-14
; OTHER INFORMATION: NT HIT: G11426714, EVALUE 1.00e-121
; US-09-864-761-32265

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Query Match          73.0%; Score 16.8; DB 10; Length 258;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAACGTGGTGGCCATTACGCT 21
Db 95 CCACTGGAGGCCATTACGCT 76

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RESULT 6
US-09-864-761-15759/c
; Sequence 15758, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15758
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002093.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.5
; NAME/KEY: unsure
; LOCATION: 256
; US-09-864-761-15758

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Query Match          73.0%; Score 16.8; DB 10; Length 454;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAACGTGGTGGCCATTACGCT 21
Db 376 CCACTGGAGGCCATTACGCT 357

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RESULT 7
US-09-360-352-11802/c
; Sequence 11802, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C

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Mon Apr 21 10:30:11 2003

us-09-270-437d-12.rnpb

; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11802
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 50-LIB34-078-Q1-E1-E10
US-09-960-352-11802

Query Match 72.2%; Score 16.6; DB 10; Length 453;
Best Local Similarity 82.6%; Pred. No. 77;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
DB 331 CCAACTGGTGGCCAGTCCAGCTCC 309

RESULT 8
US-09-864-761-13431/c
; Sequence 13431, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13431
; LENGTH: 510

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC023314.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
US-09-864-761-13431

Query Match 72.2%; Score 16.6; DB 10; Length 510;
Best Local Similarity 82.6%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
DB 351 CCAACTGGTGGCCATTGAGCATC 329

RESULT 9
US-09-873-637-1/c
; Sequence 1, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-873-637-1

Query Match 72.2%; Score 16.6; DB 10; Length 2224;
Best Local Similarity 82.6%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
DB 563 CCAGTTGATGGCCATTGAGCTTC 541

RESULT 10
US-09-864-761-21356
; Sequence 21356, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13431
; LENGTH: 510

; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
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 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 21356
 ; LENGTH: 709
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC004230.1
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 68
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.9
 ; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 5.8
 ; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 12
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 51
 ; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 45
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.2
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6
 ; OTHER INFORMATION: NT HIT: M80902.1, EVALUE 0.00e+00
 ; OTHER INFORMATION: EST HUMAN HIT: AW946377.1, EVALUE 0.00e+00
 ; OTHER INFORMATION: SWISSPROT HIT: G11351900, EVALUE 8.00e-89

Query Match 70.4%; Score 16.2; DB 10; Length 709;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AACTGGTGGCCATTACGCTTC 23
 ||||| ||||| ||||| ||||| |||||
 DB 52 AACTGGGGGGCCCTTCAGCTTC 72

RESULT 11
 ; Sequence 1201, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1201
 ; LENGTH: 1632
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-1201

Query Match 70.4%; Score 16.2; DB 9; Length 1632;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AACTGGTGGCCATTACGCTTC 23
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 DB 375 AGCTTGTGGCCATTACGCTTC 355

RESULT 12
 ; US-09-864-761-4614
 ; Sequence 4614, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aecomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
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 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 4614
 ; LENGTH: 1994
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

us-09-270-437d-12.rnpb

Mon Apr 21 10:30:11 2003

OTHER INFORMATION: MAP TO AC004230.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 68
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 51
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 45
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 37
US-09-864-761-4614

Query Match 70.4%; Score 16.2; DB 10; Length 1994;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CCACTGGTGGCCATTTCAGCTTC 23
Db 319 AACTGGGGCCCTTCAGCTTC 339

RESULT 13
US-09-372-348-14/c

Sequence 14, Application US/09372348A
Publication No. US20030028005A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Luquan
APPLICANT: Zlotnik, Albert
APPLICANT: Murgolo, Nicholas R.
APPLICANT: Greene, Jonathan R.
APPLICANT: Johnston, James A.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
FILE REFERENCE: DX0884K(2d)
CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 14
LENGTH: 2244
TYPE: DNA
ORGANISM: primate
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2244)
US-09-372-348-14

Query Match 70.4%; Score 16.2; DB 9; Length 2244;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCACTGGTGGCCATTTCAGCTTC 21
Db 2047 CCACCTGCTGGCCATTTCACCT 2027

RESULT 14

US-09-938-842A-1478
Sequence 1478, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1478
LENGTH: 2418
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1478

Query Match 70.4%; Score 16.2; DB 9; Length 2418;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCACTGGTGGCCATTTCAGCTTC 21
Db 46 CCACTGGTGGCTATGCAGCT 66

RESULT 15

US-10-261-482-3/c
Sequence 3, Application US/10261482
Publication No. US20030036089A1
GENERAL INFORMATION:
APPLICANT: Wei, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000869CON
CURRENT APPLICATION NUMBER: US/10/261,482
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 09/684,393
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: 60/172,600
PRIOR FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8001
TYPE: DNA
ORGANISM: Human
US-10-261-482-3

Query Match 70.4%; Score 16.2; DB 9; Length 8001;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AACTGGTGGCCATTTCAGCTTC 23
Db 1181 AACTGGGGGCACTCAGCTTC 1161

Search completed: April 18, 2003, 10:14:07
Job time : 97.6515 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 05:48:17 ; Search time 1266.05 Seconds
(without alignments)
456.759 Million cell updates/sec

Title: US-09-270-437D-12

Perfect score: 23

Sequence: 1 ccaactgggtggtcattcagcttc 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 32: /cgn2_6/ptodata/1/pna/US098A COMB.seq.*
- 33: /cgn2_6/ptodata/1/pna/US098B COMB.seq.*
- 34: /cgn2_6/ptodata/1/pna/US098C COMB.seq.*
- 35: /cgn2_6/ptodata/1/pna/US099A COMB.seq.*
- 36: /cgn2_6/ptodata/1/pna/US099B COMB.seq.*
- 37: /cgn2_6/ptodata/1/pna/US099C COMB.seq.*
- 38: /cgn2_6/ptodata/1/pna/US099D COMB.seq.*
- 39: /cgn2_6/ptodata/1/pna/US100A COMB.seq.*
- 40: /cgn2_6/ptodata/1/pna/US100B COMB.seq.*
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- 42: /cgn2_6/ptodata/1/pna/US101B COMB.seq.*
- 43: /cgn2_6/ptodata/1/pna/US102A COMB.seq.*
- 44: /cgn2_6/ptodata/1/pna/US102B COMB.seq.*

- 44: /cgn2_6/ptodata/1/pna/US6000 COMB.seq.*
- 45: /cgn2_6/ptodata/1/pna/US6001 COMB.seq.*
- 46: /cgn2_6/ptodata/1/pna/US6002 COMB.seq.*
- 47: /cgn2_6/ptodata/1/pna/US6003 COMB.seq.*
- 48: /cgn2_6/ptodata/1/pna/US6004 COMB.seq.*
- 49: /cgn2_6/ptodata/1/pna/US6005 COMB.seq.*
- 50: /cgn2_6/ptodata/1/pna/US6006 COMB.seq.*
- 51: /cgn2_6/ptodata/1/pna/US6007 COMB.seq.*
- 52: /cgn2_6/ptodata/1/pna/US6008 COMB.seq.*
- 53: /cgn2_6/ptodata/1/pna/US6009 COMB.seq.*
- 54: /cgn2_6/ptodata/1/pna/US6010 COMB.seq.*
- 55: /cgn2_6/ptodata/1/pna/US6011 COMB.seq.*
- 56: /cgn2_6/ptodata/1/pna/US6012 COMB.seq.*
- 57: /cgn2_6/ptodata/1/pna/US6013 COMB.seq.*
- 58: /cgn2_6/ptodata/1/pna/US6014 COMB.seq.*
- 59: /cgn2_6/ptodata/1/pna/US6015 COMB.seq.*
- 60: /cgn2_6/ptodata/1/pna/US6016 COMB.seq.*
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- 65: /cgn2_6/ptodata/1/pna/US6021 COMB.seq.*
- 66: /cgn2_6/ptodata/1/pna/US6022 COMB.seq.*
- 67: /cgn2_6/ptodata/1/pna/US6023 COMB.seq.*
- 68: /cgn2_6/ptodata/1/pna/US6024 COMB.seq.*
- 69: /cgn2_6/ptodata/1/pna/US6025 COMB.seq.*
- 70: /cgn2_6/ptodata/1/pna/US6026 COMB.seq.*
- 71: /cgn2_6/ptodata/1/pna/US6027 COMB.seq.*
- 72: /cgn2_6/ptodata/1/pna/US6028 COMB.seq.*
- 73: /cgn2_6/ptodata/1/pna/US6029 COMB.seq.*
- 74: /cgn2_6/ptodata/1/pna/US6030 COMB.seq.*
- 75: /cgn2_6/ptodata/1/pna/US6031 COMB.seq.*
- 76: /cgn2_6/ptodata/1/pna/US6032 COMB.seq.*
- 77: /cgn2_6/ptodata/1/pna/US6033 COMB.seq.*
- 78: /cgn2_6/ptodata/1/pna/US6034 COMB.seq.*
- 79: /cgn2_6/ptodata/1/pna/US6035 COMB.seq.*
- 80: /cgn2_6/ptodata/1/pna/US6036 COMB.seq.*
- 81: /cgn2_6/ptodata/1/pna/US6037 COMB.seq.*
- 82: /cgn2_6/ptodata/1/pna/US6038 COMB.seq.*
- 83: /cgn2_6/ptodata/1/pna/US6039 COMB.seq.*
- 84: /cgn2_6/ptodata/1/pna/US6040 COMB.seq.*
- 85: /cgn2_6/ptodata/1/pna/US6041 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	23	100.0	482	56	US-60-126-246-152	Sequence 152, App
C 2	23	100.0	1708	16	US-09-270-437-5	Sequence 5, Appli
C 3	23	100.0	1708	33	US-09-899-651-5	Sequence 5, Appli
C 4	23	100.0	1738	24	US-09-625-102-2082	Sequence 2082, Ap
C 5	23	100.0	1946	16	US-09-270-437-7	Sequence 7, Appli
C 6	23	100.0	1946	33	US-09-899-651-7	Sequence 7, Appli
C 7	23	100.0	2512	23	US-09-617-182-2240	Sequence 2240, Ap
C 8	19.8	86.1	412	18	US-09-487-566-4721	Sequence 4721, Ap
C 9	19.8	86.1	412	18	US-09-487-566A-4721	Sequence 4721, Ap
C 10	19.4	84.3	235	11	US-08-792-586-517	Sequence 517, App
C 11	19.4	84.3	235	20	US-09-534-843-43302	Sequence 43302, A
C 12	18.8	81.7	246	15	US-09-107-426-998	Sequence 998, App
C 13	18.8	81.7	246	49	US-60-051-750-998	Sequence 10518, A
C 14	18.8	81.7	328	29	US-09-726-807-731	Sequence 731, App
C 15	18.8	81.7	338	8	US-08-401-791A-10518	Sequence 10518, A
C 16	18.8	81.7	338	8	US-08-401-791B-10518	Sequence 10518, A
C 17	18.8	81.7	347	25	US-09-652-121-3346	Sequence 3346, Ap
C 18	18.8	81.7	367	16	US-09-270-767-1742	Sequence 1742, Ap
C 19	18.8	81.7	367	16	US-09-270-767-17044	Sequence 17024, A
C 20	18.8	81.7	367	16	US-09-270-849B-12212	Sequence 12212, A
C 21	18.8	81.7	415	1	PCT-US01-01354-3063	Sequence 3063, Ap

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Sequence 3063, Ap
Sequence 3063, Ap
Sequence 14442, A
Sequence 213, App
Sequence 14442, A
Sequence 261, App
Sequence 5712, Ap
Sequence 205, App
Sequence 205, App
Sequence 1129, Ap
Sequence 1129, Ap
Sequence 6485, Ap
Sequence 3047, Ap
Sequence 282, App
Sequence 348, App
Sequence 1243, Ap
Sequence 298, App
Sequence 298, App
Sequence 329, App
Sequence 49, App1
Sequence 28, App1
Sequence 11836, A
Sequence 40121, A
Sequence 39753, A

ALIGNMENTS

RESULT 1
US-60-126-246-152/c
; Sequence 152, Application US/60126246
; GENERAL INFORMATION:
; APPLICANT: Hodgson, David M.
; APPLICANT: Lincoln, Stephen L.
; APPLICANT: Russo, Frank D.
; APPLICANT: Spiro, Peter A.
; APPLICANT: Banville, Steve C.
; APPLICANT: Bratcher, Shawn R.
; APPLICANT: Dufour, Gerard J.
; APPLICANT: Cohen, Howard J.
; APPLICANT: Rosen, Bruce
; APPLICANT: Shah, Purvi
; APPLICANT: Chalup, Michael S.
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Jones, Anissa L.
; APPLICANT: Yu, Jimmy Y.
; APPLICANT: Greenawalt, Lila B.
; APPLICANT: Panzer, Scott R.
; APPLICANT: Roseberry, Ana M.
; APPLICANT: Wright, Rachel J.
; TITLE OF INVENTION: MOLECULES ASSOCIATED WITH GROWTH AND DEVELOPMENT
; FILE REFERENCE: PT-0002 P
; CURRENT APPLICATION NUMBER: US/60/126,246
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PERL Program
; SEQ ID NO 152
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 39667.1
US-60-126-246-152

Query Match 100.0%; Score 23; DB 56; Length 482;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-60-126-246-152

QY 1 CCAACTGGTGGCCATTCAGCTTC 23
DB 42 CCAACTGGTGGCCATTCAGCTTC 20

RESULT 2
US-09-270-437-5/c
; Sequence 5, Application US/09270437A
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen
; TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538.1 PCT
; CURRENT APPLICATION NUMBER: US/09/270,437A
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 5
; LENGTH: 1708
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-270-437-5

Query Match 100.0%; Score 23; DB 16; Length 1708;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTCAGCTTC 23
DB 68 CCAACTGGTGGCCATTCAGCTTC 46

RESULT 3
US-09-899-651-5/c
; Sequence 5, Application US/09899651
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 5
; LENGTH: 1708
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-5

Query Match 100.0%; Score 23; DB 33; Length 1708;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTCAGCTTC 23
DB 68 CCAACTGGTGGCCATTCAGCTTC 46

RESULT 4
US-09-625-102-2082
; Sequence 2082, Application US/09625102

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; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; CURRENT APPLICATION NUMBER: PA-0026 US
; CURRENT FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 2082
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 457674.1
US-09-625-102-2082

Query Match      100.0%; Score 23; DB 24; Length 1738;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 1697 CCAACTGGTGGCCATTGAGCTTC 1719

RESULT 5
US-09-270-437-7/c
; Sequence 7, Application US/09270437A
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens
; FILE REFERENCE: LUD 5538.1 PCT
; CURRENT APPLICATION NUMBER: US/09/270.437A
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 7
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-270-437-7

Query Match      100.0%; Score 23; DB 16; Length 1946;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 306 CCAACTGGTGGCCATTGAGCTTC 284

RESULT 6
US-09-899-651-7/c
; Sequence 7, Application US/09899651
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; OTHER INFORMATION: Associated
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; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/899.651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/061.709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 7
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-7

Query Match      100.0%; Score 23; DB 33; Length 1946;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 306 CCAACTGGTGGCCATTGAGCTTC 284

RESULT 7
US-09-617-182-2240/c
; Sequence 2240, Application US/09617182
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: HUMAN FETAL THYMUS LIBRARY
; FILE REFERENCE: 1600.1145-001
; CURRENT APPLICATION NUMBER: US/09/617.182
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/143.877
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 2410
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2240
; LENGTH: 2512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-617-182-2240

Query Match      100.0%; Score 23; DB 23; Length 2512;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 747 CCAACTGGTGGCCATTGAGCTTC 725

RESULT 8
US-09-487-566-4721/c
; Sequence 4721, Application US/09487566
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
; FILE REFERENCE: P044
; CURRENT APPLICATION NUMBER: US/09/487.566
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 5506
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4721
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (163)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (282)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (313)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (387)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (402)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (412)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-487-566A-4721
Query Match 86.1%; Score 19.8; DB 18; Length 412;
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAACTGGTGGCCATTCAGCTTC 23
Db 253 CCACTGGTGGCCATTCAGCTTC 231

RESULT 9
US-09-487-566A-4721/c
; Sequence 4721, Application US/09487566A
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 44
; FILE REFERENCE: PO-44
; CURRENT APPLICATION NUMBER: US/09/487,566A
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/116,668
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 5508
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4721
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (163)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (282)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (313)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (387)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (402)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (412)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-487-566A-4721
Query Match 86.1%; Score 19.8; DB 18; Length 412;
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAACTGGTGGCCATTCAGCTTC 23
Db 253 CCACTGGTGGCCATTCAGCTTC 231

RESULT 10
US-08-792-586-517/c
; Sequence 517, Application US/08792586
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Lane, John C.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Snable, James L.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: COLON WITH CROHN'S DISEASE
; NUMBER OF SEQUENCES: 2231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,586
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/010,832
; FILING DATE: January 30, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/010,812
; FILING DATE: January 30, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 517:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 775742
; US-08-792-586-517
Query Match 84.3%; Score 19.4; DB 11; Length 235;
Best Local Similarity 95.2%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCACTGGTGGCCATTCAGCTT 22
Db 224 CCACTGGTGGCCATTCAGCTT 204

RESULT 11
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US-09-534-843-43302/c
; Sequence 43302, Application US/09534843
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLECULE
; FILE REFERENCE: PD-1007 CIP
; CURRENT APPLICATION NUMBER: US/09/534,843
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 49783
; SOFTWARE: PERL Program
; SEQ ID NO 43302
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00282360
; NAME/KEY: unsure
; LOCATION: 178, 197, 226
; OTHER INFORMATION: a, t, c, g, or other
US-09-534-843-43302

Query Match 84.3%; Score 19.4; DB 20; Length 235;
Best Local Similarity 95.2%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAACGTGGTGGCCCTTCAGCTT 22
DB 224 CAACGTGGTGGCCCTTCAGCTT 204

RESULT 12
US-09-107-426-998/c
; Sequence 998, Application US/09107426
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; NUMBER OF SEQUENCES: 1626
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,426
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0396P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 998:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 3421335H1
US-09-107-426-998

Query Match 81.7%; Score 18.8; DB 49; Length 246;
Best Local Similarity 90.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCCTTCAGCTT 22
DB 204 CCAACTGGTGGCCCTTCAGCTT 183

RESULT 14

LENGTH: 246 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 3421335H1
US-09-107-426-998

Query Match 81.7%; Score 18.8; DB 15; Length 246;
Best Local Similarity 90.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCCTTCAGCTT 22
DB 204 CCAACTGGTGGCCCTTCAGCTT 183

RESULT 13
US-60-051-750-998/c
; Sequence 998, Application US/60051750
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; NUMBER OF SEQUENCES: 1626
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/051,750
; FILING DATE: HEREWITH
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0396P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 998:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 3421335H1
US-60-051-750-998

Query Match 81.7%; Score 18.8; DB 49; Length 246;
Best Local Similarity 90.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCCTTCAGCTT 22
DB 204 CCAACTGGTGGCCCTTCAGCTT 183

us-09-270-437d-12.rnrm

Mon Apr 21 10:30:15 2003

US-09-726-807-731/c
; Sequence 731, Application US/09726807
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2053-001
; CURRENT APPLICATION NUMBER: US/09/726,807
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,040
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 4076
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 731
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Homo sapiens.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(328)
; OTHER INFORMATION: n = A,T,C or G
US-09-726-807-731

Query Match 81.7%; Score 18.8; DB 29; Length 328;
Best Local Similarity 90.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 2;

Qy 1 CCAACTGGTGGCCATTGAGCTT 22
Db 145 CCAGCTGGTGGCCCTTCAGCTT 124

RESULT 15
US-08-401-791A-10518/c
; Sequence 10518, Application US/08401791A
; GENERAL INFORMATION:
; APPLICANT: Haseltine, William
; APPLICANT: Rosen, Craig
; APPLICANT: Ruben, Steve
; APPLICANT: Dillon, Patrick
; APPLICANT: Li, Haodong
; APPLICANT: Earle-Hughes, Julie
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
; NUMBER OF SEQUENCES: 17621
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 5.0
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,791A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 325800-307
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 994-1700
; TELEFAX: (201) 994-1744
; INFORMATION FOR SEQ ID NO: 10518:

SEQUENCE CHARACTERISTICS:
; LENGTH: 338 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-401-791A-10518

Query Match 81.7%; Score 18.8; DB 8; Length 338;
Best Local Similarity 90.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGAGCTT 22
Db 227 CCAGCTGGTGGCCCTTCAGCTT 206

Search completed: April 18, 2003, 09:35:46
Job time : 1268.05 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:28 ; Search time 256.311 Seconds
(without alignments)
400.770 Million cell updates/sec

Title: US-09-270-437D-12
Perfect score: 23
Sequence: 1 ccaactgggtggccattcagcttc 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5897297 seqs, 2233080881 residues

Total number of hits satisfying chosen parameters: 11794594

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3.*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
- 10: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	23	100.0	23	US-09-270-437D-12
2	23	100.0	1708	Sequence 12, Appl
3	23	100.0	1946	Sequence 5, Appl
4	23	100.0	1990	Sequence 7, Appl
5	23	100.0	1990	Sequence 7, Appl
6	23	100.0	2040	Sequence 7, Appl
7	23	100.0	2040	Sequence 7, Appl
8	23	100.0	2069	Sequence 6, Appl
9	23	100.0	2069	Sequence 6, Appl
10	23	100.0	2119	Sequence 10, Appl
11	23	100.0	2119	Sequence 10, Appl
12	23	100.0	2158	Sequence 5, Appl
13	23	100.0	2158	Sequence 5, Appl
14	23	100.0	2208	Sequence 9, Appl
15	23	100.0	2208	Sequence 9, Appl
16	23	100.0	2427	Sequence 8, Appl
17	19.8	86.1	412	Sequence 10107, A
18	18.8	81.7	705	Sequence 212894, A
19	18.4	80.0	43537	Sequence 39653, A
20	17.8	77.4	1396	Sequence 13458, A
21	17.8	77.4	3628	Sequence 2390, Ap
22	17.8	77.4	3628	Sequence 4108, Ap
				Sequence 2117, Ap

ALIGNMENTS

RESULT 1

US-09-270-437D-12
; Sequence 12, Application US/09270437D
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen

; FILE REFERENCE: LUD 5538.1
; CURRENT APPLICATION NUMBER: US/09/270,437D
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 12
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-270-437D-12

Query Match 100.0%; Score 23; DB 5; Length 23;
Best local Similarity 100.0%; Pred. No. 0.34; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0

Qy 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 1 CCAACTGGTGGCCATTGAGCTTC 23

RESULT 2

US-09-270-437D-5/c
; Sequence 5, Application US/09270437D
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander

Sequence 4108, Ap
Sequence 41211, A
Sequence 9790, Ap
Sequence 21037, A
Sequence 5222, Ap
Sequence 20973, A
Sequence 9654, Ap
Sequence 9630, Ap
Sequence 9990, Ap
Sequence 33068, A
Sequence 33079, A
Sequence 33071, A
Sequence 135882, A
Sequence 135883, A
Sequence 135884, A
Sequence 135885, A
Sequence 1297, Ap
Sequence 18990, A
Sequence 13, Appl
Sequence 233, Appl
Sequence 17364, A

us-09-270-437d-12.rnpn

Mon Apr 21 10:30:17 2003

APPLICANT: Old, Lloyd J.
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen
 FILE REFERENCE: LUD 538.1
 CURRENT APPLICATION NUMBER: US/09/270,437D
 CURRENT FILING DATE: 1999-03-16
 PRIOR APPLICATION NUMBER: 09/061,709
 PRIOR FILING DATE: 1998-04-17
 NUMBER OF SEQ ID NOS: 23
 SEQ ID NO 5
 LENGTH: 1708
 TYPE: DNA
 ORGANISM: Homo sapiens
 NAME/KEY: CDS
 LOCATION: 1384,1464,1533,1571,1595
 OTHER INFORMATION: unsure of nucleotide
 US-09-270-437D-5

Query Match 100.0%; Score 23; DB 5; Length 1708;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
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 DB 68 CCAACTGGTGGCCATTGAGCTTC 46

RESULT 3
 US-09-270-437D-7/c
 Sequence 7, Application US/09270437D
 GENERAL INFORMATION:
 APPLICANT: Chen, Yao-Tseung
 APPLICANT: Gure, Ali
 APPLICANT: Tsang, Solam
 APPLICANT: Stockert, Elisabeth
 APPLICANT: Jager, Elke
 APPLICANT: Knuth, Alexander
 APPLICANT: Old, Lloyd J.
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen
 FILE REFERENCE: LUD 538.1
 CURRENT APPLICATION NUMBER: US/09/270,437D
 CURRENT FILING DATE: 1999-03-16
 PRIOR APPLICATION NUMBER: 09/061,709
 PRIOR FILING DATE: 1998-04-17
 NUMBER OF SEQ ID NOS: 23
 SEQ ID NO 7
 LENGTH: 1946
 TYPE: DNA
 ORGANISM: Homo sapiens
 NAME/KEY: CDS
 LOCATION: 1622,1702,1771,1809,1833
 OTHER INFORMATION: unsure of nucleotide
 US-09-270-437D-7

Query Match 100.0%; Score 23; DB 5; Length 1946;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
 |||||
 DB 306 CCAACTGGTGGCCATTGAGCTTC 284

RESULT 4
 US-09-724-676-7/c
 Sequence 7, Application US/09724676
 GENERAL INFORMATION:
 APPLICANT: Compugen LTD
 TITLE OF INVENTION: Variants of alternative splicing
 FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676
 CURRENT FILING DATE: 2000-11-28
 NUMBER OF SEQ ID NOS: 97222
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 7
 LENGTH: 1990
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-724-676-7

Query Match 100.0%; Score 23; DB 6; Length 1990;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
 |||||
 DB 442 CCAACTGGTGGCCATTGAGCTTC 420

RESULT 5
 US-09-724-676A-7/c
 Sequence 7, Application US/09724676A
 GENERAL INFORMATION:
 APPLICANT: Compugen LTD
 TITLE OF INVENTION: Variants of alternative splicing
 FILE REFERENCE: 129181.4 Compugen
 CURRENT APPLICATION NUMBER: US/09/724,676A
 CURRENT FILING DATE: 2000-11-28
 NUMBER OF SEQ ID NOS: 97222
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 7
 LENGTH: 1990
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-724-676A-7

Query Match 100.0%; Score 23; DB 6; Length 1990;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
 |||||
 DB 442 CCAACTGGTGGCCATTGAGCTTC 420

RESULT 6
 US-09-724-676-6/c
 Sequence 6, Application US/09724676
 GENERAL INFORMATION:
 APPLICANT: Compugen LTD
 TITLE OF INVENTION: Variants of alternative splicing
 FILE REFERENCE: 129181.4 Compugen
 CURRENT APPLICATION NUMBER: US/09/724,676
 CURRENT FILING DATE: 2000-11-28
 NUMBER OF SEQ ID NOS: 97222
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 6
 LENGTH: 2040
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-724-676-6

Query Match 100.0%; Score 23; DB 6; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
 |||||
 DB 442 CCAACTGGTGGCCATTGAGCTTC 420

RESULT 7
 US-09-724-676A-6/c

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; Sequence 6, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-6

Query Match      100.0%; Score 23; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
|||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

RESULT 8
US-09-724-676-10/c
; Sequence 10, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-10

Query Match      100.0%; Score 23; DB 6; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
|||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

RESULT 9
US-09-724-676A-10/c
; Sequence 10, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-10

Query Match      100.0%; Score 23; DB 6; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
|||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

RESULT 10
US-09-724-676-5/c
; Sequence 5, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 2119
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-5

Query Match      100.0%; Score 23; DB 6; Length 2119;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
|||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

RESULT 11
US-09-724-676A-5/c
; Sequence 5, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 2119
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-5

Query Match      100.0%; Score 23; DB 6; Length 2119;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
|||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

RESULT 12
US-09-724-676-9/c
; Sequence 9, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-9

Query Match      100.0%; Score 23; DB 6; Length 2158;
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us-09-270-437d-12.rnpn

Mon Apr 21 10:30:17 2003

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-8

Query Match      100.0%; Score 23; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
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DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-9/c

Query Match      100.0%; Score 23; DB 6; Length 2158;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
    |||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-9

Query Match      100.0%; Score 23; DB 6; Length 2158;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
    |||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-8/c

Query Match      100.0%; Score 23; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
    |||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-8/c

Query Match      100.0%; Score 23; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
    |||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

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```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-8/c

Query Match      100.0%; Score 23; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
    |||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

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```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-8/c

Query Match      100.0%; Score 23; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
    |||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-8/c

Query Match      100.0%; Score 23; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
    |||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

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```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-8/c

Query Match      100.0%; Score 23; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
    |||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-8/c

Query Match      100.0%; Score 23; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGCTTC 23
    |||||
DB 442 CCAACTGGTGGCCATTGAGCTTC 420

Search completed: April 18, 2003, 10:50:27
Job time : 257.311 secs

```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:47:40 ; Search time 800.818 Seconds
(without alignments)
465.145 Million cell updates/sec

Title: .US-09-270-437D-12

Perfect score: 23

Sequence: 1 ccaactgggtggccattcagcttc 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vit:*

22: em_gss_fun:*

23: em_gss_man:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	23	100.0	249	9	AA196774
C 2	23	100.0	466	9	AA196976
C 3	23	100.0	764	13	BM006191
C 4	23	100.0	877	12	BG473949
C 5	23	100.0	896	14	BQ647425
C 6	23	100.0	929	14	BQ652586

C 7	23	100.0	940	14	BQ649666
C 8	23	100.0	950	14	BQ648383
C 9	23	100.0	953	14	BQ647360
C 10	23	100.0	955	14	BQ651665
C 11	23	100.0	982	14	BQ652180
C 12	23	100.0	983	14	BQ643920
C 13	23	100.0	1042	14	BM928196
C 14	23	100.0	1061	14	BQ647561
C 15	21.4	93.0	770	10	BE541467
C 16	19.4	84.3	912	17	B08385
C 17	18.8	81.7	326	13	BM148903
C 18	18.8	81.7	352	17	AQ132664
C 19	18.8	81.7	505	13	BM146309
C 20	18.8	81.7	589	12	BG025694
C 21	18.8	81.7	641	12	B797894
C 22	18.8	81.7	844	17	AZ901563
C 23	18.8	81.7	1095	13	BM475738
C 24	18.2	79.1	155	17	BH315184
C 25	18.2	79.1	433	10	BE508123
C 26	18.2	79.1	508	12	BG407307
C 27	18.2	79.1	528	13	BI348247
C 28	18.2	79.1	588	13	BI446082
C 29	18.2	79.1	719	17	BH444983
C 30	18.2	79.1	776	17	BH054219
C 31	17.8	77.4	325	10	AV952715
C 32	17.8	77.4	414	17	AZ762364
C 33	17.8	77.4	482	13	BI401056
C 34	17.8	77.4	551	17	B26736
C 35	17.8	77.4	552	10	BE231931
C 36	17.8	77.4	570	14	BQ603654
C 37	17.8	77.4	604	10	AV825598
C 38	17.8	77.4	621	9	AL683579
C 39	17.8	77.4	634	9	AL595504
C 40	17.8	77.4	657	9	AU237120
C 41	17.8	77.4	682	9	AL640616
C 42	17.8	77.4	724	12	BF307752
C 43	17.8	77.4	796	17	BI1822
C 44	17.4	75.7	401	17	AZ000183
C 45	17.4	75.7	597	17	AQ482316

ALIGNMENTS

RESULT 1
AA196774/c
LOCUS
DEFINITION
zq60f02.r1 Stratagene neuroepithelium (#937231) Homo sapiens CDNA
clone IMAGE:646011 5', mRNA sequence.
ACCESSION
AA196774
VERSION
AA196774.1 GI:1792476
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 249)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.,
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

249 bp mRNA linear EST 22-JAN-1997
zq60f02.r1 Stratagene neuroepithelium (#937231) Homo sapiens CDNA
clone IMAGE:646011 5', mRNA sequence.

AA196774.1 GI:1792476

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 249)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,

B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,

Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.,

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

BQ649666 AGENCOURT
BQ648383 AGENCOURT
BQ647360 AGENCOURT
BQ651665 AGENCOURT
BQ652180 AGENCOURT
BQ643920 AGENCOURT
BM928196 AGENCOURT
BQ647561 AGENCOURT
BE541467 601067919
B08385 F18A15-T7.1
BM148903 TCARP2852
AQ132664 HS 3058_A
BM146309 TCARP1543
BG025694 602274861
BF797894 602257293
AZ901563 RPCI-24-2
BM475738 AGENCOURT
BH315184 CH230-209
BE508123 dc36h02.y
BG407307 dabi7B05.
BI348247 dabi7B07.
BI446082 dabi35908.
BH444983 BOHQB46TR
BH054219 RPCI-24-3
AV952715 AV952715
AZ762364 LM0557P21
BI401056 MI-P-CP0-
B26736 T18CT7F TAM
BE231931 136808 MA
BQ603654 MI-P-CP0-
AV825598 AV825598
AL683579 AL683579
AL595504 AL595504
AU237120 AU237120
AL640616 AL640616
BF307752 601890820
BI1822 F18A15-T7.3
AZ000183 RPCI-23-3
AQ482316 RPCI-11-2

US-09-270-437d-12.rst

Mon Apr 21 10:30:18 2003

cells (Ntera-2/ci.D1) induced with Retinoic Acid for 24 hours. Average insert size: 1.5 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATCGGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3' others

BASE COUNT 121 a 123 c 124 g 87 t 11 others

FEATURES source

1. .249
/organism="Homo sapiens"
/db_xref="GDB:5216262"
/db_xref="taxon:9606"
/clone="IMAGE:646011"
/clone_lib="Stratagene neuroepithelium (#937231)"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/note="vector: pBluescript SK-; Site 1: ECORI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2 cells (Ntera-2/ci.D1) induced with Retinoic Acid for 24 hours. Average insert size: 1.5 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATCGGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3' others

BASE COUNT 56 a 71 c 73 g 43 t 6 others

Query Match 100.0%; Score 23; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.8; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 1 CCAACTGGTGGCCATTCAGCTTC 23
DB 42 CCAACTGGTGGCCATTCAGCTTC 20

RESULT 2
AA196976/c 456 bp mRNA linear EST 22-JAN-1997
LOCUS zq60h02.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA
DEFINITION clone IMAGE:646035 5', mRNA sequence.

ACCESSION AA196976
VERSION AA196976.1 GI:1792567
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 466)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Pavello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfsing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Weg, J., Trevaakis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 167.

FEATURES source

1. .466
/organism="Homo sapiens"
/db_xref="GDB:5216262"
/db_xref="taxon:9606"
/clone="IMAGE:646035"
/clone_lib="Stratagene neuroepithelium (#937231)"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/note="vector: pBluescript SK-; Site 1: ECORI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2

Query Match 100.0%; Score 23; DB 9; Length 466;
Best Local Similarity 100.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 1 CCAACTGGTGGCCATTCAGCTTC 23
DB 42 CCAACTGGTGGCCATTCAGCTTC 20

RESULT 3
BM006191/c 764 bp mRNA linear EST 30-OCT-2001
LOCUS 603614013F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5433698 5',
DEFINITION mRNA sequence.

ACCESSION BM006191
VERSION BM006191.1 GI:16520545
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 764)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: CGAP (Stanford)
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
DNA Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1909 row: j column: 03
High quality sequence stop: 756.

FEATURES source

Location/Qualifiers
1. .764
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5433698"
/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2: ECORI; cDNA made by oligo-dt priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin. (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
198 a 209 c 217 g 140 t

BASE COUNT 198 a 209 c 217 g 140 t

ORIGIN

Query Match 100.0%; Score 23; DB 13; Length 764;
Best Local Similarity 100.0%; Pred. No. 4.6; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 1 CCAACTGGTGGCCATTCAGCTTC 23
DB 45 CCAACTGGTGGCCATTCAGCTTC 23

RESULT 4

BG473949/c
 LOCUS BG473949 877 bp mRNA linear EST 21-MAR-2001
 DEFINITION 602516444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4647994 5',
 mRNA sequence.
 ACCESSION BG473949
 VERSION BG473949.1 GI:13406226
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 877)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Cloned into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC Library.
 found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLC1425 row: h column: 11
 High quality sequence stop: 673.
 Location/Qualifiers
 1..877
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4647994"
 /clone_lib="NIH_MGC_16"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 205 a 269 c 257 g 146 t
 ORIGIN
 Query Match 100.0%; Score 23; DB 12; Length 877;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCAACTGGTGGCCATTCAGCTTC 23
 Db 690 CCAACTGGTGGCCATTCAGCTTC 668
 RESULT 5
 BG647425/c
 LOCUS BG647425 896 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT_8346875 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6283876
 5', mRNA sequence.
 ACCESSION BG647425
 VERSION BG647425.1 GI:21771597
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 896)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Cloned into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC Library.
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCW2497 row: k column: 24
 High quality sequence stop: 533.
 Location/Qualifiers
 1..929
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6293903"
 /clone_lib="NIH_MGC_100"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Cloned into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library.
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2480 row: j column: 05
 High quality sequence stop: 421.
 Location/Qualifiers
 1..896
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6283876"
 /clone_lib="NIH_MGC_100"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."
 BASE COUNT 255 a 235 c 252 g 150 t 4 others
 ORIGIN
 Query Match 100.0%; Score 23; DB 14; Length 896;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCAACTGGTGGCCATTCAGCTTC 23
 Db 354 CCAACTGGTGGCCATTCAGCTTC 332
 RESULT 6
 BG652586/c
 LOCUS BG652586 929 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT_8490818 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6293903
 5', mRNA sequence.
 ACCESSION BG652586
 VERSION BG652586.1 GI:21776758
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 929)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Cloned into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC Library.
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCW2497 row: k column: 24
 High quality sequence stop: 533.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6293903"
 /clone_lib="NIH_MGC_100"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 260 a 264 g 158 t
ORIGIN

Query Match 100.0%; Score 23; DB 14; Length 929;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 417 CCAACTGGTGGCCATTGAGCTTC 395

RESULT 7
BQ649666/c
LOCUS
DEFINITION BQ649666 940 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8286221 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6299693
5', mRNA sequence.

ACCESSION BQ649666
VERSION BQ649666.1 GI:21773838
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 940)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2512 row: m column: 06
High quality sequence stop: 395.

FEATURES
source

1..940
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6299693"
/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 258 a 269 c 262 g 149 t
ORIGIN

Query Match 100.0%; Score 23; DB 14; Length 940;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 337 CCAACTGGTGGCCATTGAGCTTC 315

RESULT 8
BQ648383/c
LOCUS

DEFINITION BQ648383 950 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8342265 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6268202
5', mRNA sequence.

ACCESSION BQ648383
VERSION BQ648383.1 GI:21772555
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 950)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2439 row: m column: 03
High quality sequence stop: 599.

FEATURES
source

1..950
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6268202"
/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 237 a 278 c 269 g 166 t
ORIGIN

Query Match 100.0%; Score 23; DB 14; Length 950;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAACTGGTGGCCATTGAGCTTC 23
Db 43 CCAACTGGTGGCCATTGAGCTTC 21

RESULT 9
BQ647360/c
LOCUS
DEFINITION BQ647360 953 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8443628 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6284231
5', mRNA sequence.

ACCESSION BQ647360
VERSION BQ647360.1 GI:21771532
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 953)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2481 row: h column: 24
High quality sequence stop: 651.
Location/Qualifiers

FEATURES

source

1. .953
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6284231"
/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 277 a 251 c 258 g 166 t 1 others
ORIGIN

Query Match 100.0%; Score 23; DB 14; Length 953;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGACGCTTC 23
|||||
DB 336 CCAACTGGTGGCCATTGACGCTTC 314

RESULT 10
BQ651665/c

LOCUS BQ651665
DEFINITION AGENCOURT 8297761 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6269842
5', mRNA sequence.
ACCESSION BQ651665
VERSION BQ651665.1 GI:21775837
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 955)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

FEATURES

source

High quality sequence stop: 588.
Location/Qualifiers
1. .955
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6269842"

/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 232 a 313 c 253 g 157 t
ORIGIN

Query Match 100.0%; Score 23; DB 14; Length 955;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGACGCTTC 23
|||||
DB 43 CCAACTGGTGGCCATTGACGCTTC 21

RESULT 11

BQ652180/c

LOCUS BQ652180
DEFINITION AGENCOURT 8188778 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6282804
5', mRNA sequence.
ACCESSION BQ652180
VERSION BQ652180.1 GI:21776352
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 982)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2477 row: m column: 13
High quality sequence stop: 667.
Location/Qualifiers

FEATURES

source

1. .982
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6282804"
/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 292 a 251 c 267 g 170 t 2 others
ORIGIN

Query Match

Best Local Similarity 100.0%; Score 23; DB 14; Length 982;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-270-437d-12.rst

Mon Apr 21 10:30:18 2003

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGTTC 23
 Db 336 CCAACTGGTGGCCATTGAGTTC 314

RESULT 12
 BQ643920/c 983 bp mRNA linear EST 15-JUL-2002
 LOCUS AGENCOURT 8303966 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6269413
 DEFINITION 5', mRNA sequence.

ACCESSION BQ643920
 VERSION BQ643920.1 GI:21768092
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 983)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

FEATURES
 source
 1..983
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone="IMAGE:6269413"
 /clone_lib="NIH_MGC_100"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="PH108 (phage-resistant)"
 /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." Plate: LLCM2442 row: 0 column: 14 High quality sequence stop: 491.
 Location/Qualifiers

BASE COUNT 256 a 279 c 274 g 174 t
 ORIGIN

Query Match 100.0%; Score 23; DB 14; Length 983;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGTTC 23
 Db 43 CCAACTGGTGGCCATTGAGTTC 21

RESULT 13
 BM928196/c 1042 bp mRNA linear EST 12-MAR-2002
 LOCUS AGENCOURT 6715416 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5797961
 DEFINITION 5', mRNA sequence.

ACCESSION BM928196
 VERSION BM928196.1 GI:19378575
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1061)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

FEATURES
 source
 1..1042
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone="IMAGE:5797961"
 /clone_lib="NIH_MGC_100"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." Plate: LLCM2025 row: c column: 18 High quality sequence stop: 662.
 Location/Qualifiers

BASE COUNT 266 a 299 c 286 g 190 t
 ORIGIN

Query Match 100.0%; Score 23; DB 14; Length 1042;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTGAGTTC 23
 Db 43 CCAACTGGTGGCCATTGAGTTC 21

RESULT 14
 BQ647561/c 1061 bp mRNA linear EST 15-JUL-2002
 LOCUS AGENCOURT 8349614 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6284767
 DEFINITION 5', mRNA sequence.

ACCESSION BQ647561
 VERSION BQ647561.1 GI:21771733
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1061)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

FEATURES
 source
 1..1042
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone="IMAGE:5797961"
 /clone_lib="NIH_MGC_100"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." Plate: LLCM2482 row: 0 column: 08 High quality sequence stop: 443.

FEATURES
source

Location/Qualifiers
 1. .1061
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6284767"
 /clone_lib="NIH_MGC_100"
 /tissue_type="Hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /notes="Organ: liver; Vector: pOPB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 277 a 323 c 282 g 179 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 23; DB 14; Length 1061;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAACTGGTGGCCATTCAGCTTC 23
 |||||
 Db 43 CCAACTGGTGGCCATTCAGCTTC 21

RESULT 15
BE541467/c

LOCUS BE541467 770 bp mRNA linear EST 09-AUG-2000
 DEFINITION 601067919F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454085 5',
 mRNA sequence.
 ACCESSION BE541467
 VERSION BE541467.1 GI:9770112
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: sgapsb@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM8438 row: f column: 06
 High quality sequence stop: 631.
 Location/Qualifiers
 1. .770

FEATURES
source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3454085"
 /clone_lib="NIH_MGC_10"
 /cell_line="MGC36"
 /lab_host="DH10B"
 /notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 Kb. Library prepared by Life Technologies."
 221 a 210 c 224 g 115 t

BASE COUNT
ORIGIN

Query Match 93.0%; Score 21.4; DB 10; Length 770;
 Best Local Similarity 95.7%; Pred. No. 25;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCAACTGGTGGCCATTCAGCTTC 23
 |||||
 Db 305 CCCACTGGTGGCCATTCAGCTTC 283

Search completed: April 18, 2003, 07:31:57
 Job time : 804.985 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:46:26 ; Search time 292 Seconds
(without alignments)
2192.677 Million cell updates/sec

Title: US-09-270-437D-13
Perfect score: 22
Sequence: 1 gctcttgggacaggaagtc 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.ste.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.ste.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.in.*
- 32: em.htg.inv.*
- 33: em.htg.other.*
- 34: em.htg.mus.*
- 35: em.htg.pin.*
- 36: em.htg.rod.*
- 37: em.htg.mam.*
- 38: em.htg.vrt.*
- 39: em.sy.*
- 40: em.htgo.hum.*
- 41: em.htgo.mus.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	21	95.5	198623	2	AC113611	AC113611 Homo sapi
2	20	90.9	184582	2	AC105949	AC105949 Mus muscu
3	19.4	88.2	2010	9	AF117107	AF117107 Homo sapi
4	19.4	88.2	2935	6	AR059699	AR059699 Sequence
5	19.4	88.2	2935	6	AR083389	AR083389 Sequence
6	19.4	88.2	2935	6	AR164498	AR164498 Sequence
7	19.4	88.2	2935	6	I15470	I15470 Sequence 1
8	19.4	88.2	2935	6	I32484	I32484 Sequence 1
9	19.4	88.2	3283	6	ARI171867	ARI171867 Sequence
10	19.4	88.2	3412	6	ARI171865	ARI171865 Sequence
11	19.4	88.2	3642	9	BC021290	BC021290 Homo sapi
12	19.4	88.2	3667	9	AF057352	AF057352 Homo sapi
13	19.4	88.2	91084	9	AL596177	AL596177 Human DNA
14	19.4	88.2	112259	2	AC026579	AC026579 Homo sapi
15	19.4	88.2	142971	9	AC020629	AC020629 Homo sapi
16	19.4	88.2	146376	9	AC009247	AC009247 Homo sapi
17	19.4	88.2	150595	2	AC095143	AC095143 Rattus no
18	19.4	88.2	181007	2	AC118527	AC118527 Rattus no
19	19.4	88.2	182695	2	AC015706	AC015706 Homo sapi
20	19.4	88.2	193422	2	AC068664	AC068664 Mus muscu
21	19.4	88.2	214592	2	AC084163	AC084163 Mus muscu
22	19.4	88.2	214823	2	AC113869	AC113869 Rattus no
23	19.4	86.4	139351	2	AC129792	AC129792 Rattus no
24	19.4	85.4	167686	2	AC113909	AC113909 Rattus no
25	18.8	85.5	2786	9	AK096182	AK096182 Homo sapi
26	18.8	85.5	7085	8	AF231351	AF231351 Nicotiana
27	18.8	85.5	110000	2	AC021072	Continuation (2 of
28	18.8	85.5	141594	9	AC068302	AC068302 Homo sapi
29	18.8	85.5	190588	2	AC009861	AC009861 Homo sapi
30	18.8	85.5	190610	2	AC130419	AC130419 Homo sapi
31	18.4	83.6	2517	9	AK096200	AK096200 Homo sapi
32	18.4	83.6	57100	2	AC100002	AC100002 Mus muscu
33	18.4	83.6	155301	9	AC041040	AC041040 Homo sapi
34	18.4	83.6	156442	9	AC107385	AC107385 Homo sapi
35	18.4	83.6	174007	8	OSJN00181	OSJN00181 Homo sapi
36	18.4	83.6	186517	9	AC022710	AL662983 Oryza sat
37	18.4	83.6	205998	9	AC113187	AC113187 Homo sapi
38	18.4	83.6	207438	2	AC110819	AC110819 Mus muscu
39	18.4	83.6	237732	2	AC125117	AC125117 Mus muscu
40	18.4	83.6	271144	9	HSXDPB	AC113187 Homo sapi
41	18.4	83.6	330999	2	AC009583	AL590763 Homo sapi
42	18.4	81.8	116304	9	AL139411	AC009583 Homo sapi
43	18.4	81.8	155157	2	AL359549	AL139411 Human DNA
44	18.4	81.8	165524	2	AC129304	AL359549 Homo sapi
45	18.4	81.8	176046	9	AC073366	AC129304 Mus muscu
						AC073366 Homo sapi

ALIGNMENTS

RESULT 1
AC113611
LOCUS
DEFINITION Homo sapiens chromosome 4 clone RP11-421M20, WORKING DRAFT
AC113611
SEQUENCE, 4 unordered pieces.
ACCESSION AC113611.2 GI:20136967
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEPIN.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 198623)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone

Unpublished
2 (bases 1 to 198623)
Waterston,R.H.
Direct Submission
Submitted (04-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 198623)
Waterston,R.H.
Direct Submission
Submitted (11-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Apr 11, 2002 this sequence version replaced gi:19073839.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.edu
----- Project Information -----
Center project name: H.NH0421M20
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-primer ET; 0% of reads
Assembly: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 189380 bases at least Q40
Consensus quality: 189735 bases at least Q30
Consensus quality: 199273 bases at least Q20
Insert size: 196000; agarose-fp
Insert size: 206234; sum-of-contigs
Quality coverage: 8.84 in Q20 bases; agarose-fp
Quality coverage: 8.97 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 26542: contig of 26542 bp in length
* 26543 26642: gap of unknown length
* 26543 57247: contig of 30605 bp in length
* 57248 57347: gap of unknown length
* 108935 108935: contig of 51588 bp in length
* 108936 109035: gap of unknown length
* 109036 198623: contig of 89588 bp in length.
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* Location/Qualifiers
* 1..198623
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="4"
* /clone="RP11-421M20"
* 1..26542
* /note="assembly_name:Contig12"
* 26643..57247
* /note="assembly_name:Contig13
* clone_end:SP6
* vector_side:right"
* 57348..108935
* /note="assembly_name:Contig14
* clone_end:T7
* vector_side:right"
* 109036..198623
* /note="assembly_name:Contig15"
* 47163 a 53839 c 54375 g 42946 t 300 others

BASE COUNT
ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 198623;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTTTGGGACAGGAGGT 21
DB 9880 GCTCTTTGGGACAGGAGGT 9900

RESULT 2
AC105949 184582 bp DNA linear HTG 14-APR-2002
LOCUS Mus musculus clone RP24-217C15, WORKING DRAFT SEQUENCE, 12 ordered
DEFINITION pieces.
ACCESSION AC105949
VERSION AC105949.2 GI:20147936
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 184582)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP24-217C15
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 184582)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kanat,A., Kazatas,A., Kellis,C., Lakocque,K.,
Lanazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Major,J., McKernan,K., McPheeters,R., Meldrim,J.,
McCarthy,M., McEwan,P., McKernan,K., Murphy,T., Naylor,J., Nguyen,C.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., O'Donnell,P., O'Neil,D.,
Norbu,C., Norman,C.H., O'Connor,T., Phunkhang,P., Pierre,N., Pollara,V.,
Oliver,J., Peterson,K., Phunkhang,P., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

DIRECT SUBMISSION
Submitted (11-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 184582)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepe,Y., Colangelo,M., Collins,S., Collymore,A.,
Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kanat,A., Kazatas,A., Kellis,C., Lakocque,K., Lanazares,R.,
Lanazares,R., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., McKernan,K., McPheeters,R.,
McCarthy,M., McEwan,P., McKernan,K., Murphy,T., Naylor,J., Nguyen,C.,
Mihova,T., Mlenga,V., Murphy,T., O'Donnell,P., O'Neil,D.,
Norbu,C., Norman,C.H., O'Connor,T., Phunkhang,P., Pierre,N., Pollara,V.,
Oliver,J., Peterson,K., Phunkhang,P., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 14, 2002 this sequence version replaced gi:18129448.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information -----
Center project name: L18821
Center clone name: 217 C 15

----- Summary Statistics -----
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 181431 bases at least Q40
Consensus quality: 182839 bases at least Q30
Consensus quality: 183305 bases at least Q20

Insert size: 183000; agarose-fp
Insert size: 183482; sum-of-contigs

Quality coverage: 6.9 in Q20 bases; agarose-fp
Quality coverage: 6.9 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 1013: contig of 1013 bp in length
1014 1113: gap of 100 bp
1114 2223: contig of 1110 bp in length
2224 2323: gap of 100 bp
2324 4327: contig of 2004 bp in length
4328 4427: gap of 100 bp
4428 6625: contig of 2198 bp in length
6626 6725: gap of 100 bp
6726 10232: contig of 3507 bp in length
10233 10332: gap of 100 bp
10333 17741: contig of 7409 bp in length
17742 17841: gap of 100 bp
17842 30472: contig of 12631 bp in length
30473 30572: gap of 100 bp
30573 49894: contig of 19322 bp in length
49895 49994: gap of 100 bp
49995 69993: contig of 19999 bp in length
69994 70093: gap of 100 bp
70094 89184: contig of 19091 bp in length
89185 89284: gap of 100 bp
89285 106186: contig of 16902 bp in length
106187 106286: gap of 100 bp
106287 184582: contig of 78296 bp in length.

FEATURES

source

1. .184582
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="RP24-217C15"
/clone_lib="RP24-217C15"
1. .1013
/notes="assembly_fragment"
1114. .2223
/notes="assembly_fragment"
2224. .4327
/notes="assembly_fragment"
4428. .6625

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature
6726. .10232
/notes="assembly_fragment"
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10333. .17741
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misc_feature
17842. .30472
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30573. .49894
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49995. .69993
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70094. .89184
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misc_feature
89285. .106186
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106287. .184582
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BASE COUNT 53205 a 38803 c 37801 g 53673 t 1100 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTTGGGACAGGAGG 20
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Db 139851 GCCTTTGGGACAGGAGG 139870

RESULT 3

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

misc_feature

CDS

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misc_feature

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      Jones, S. and Tang, J.
TITLE       Calcium independent cytosolic phospholipase A.sub.2 /B enzymes
JOURNAL     Patent: US 5589170-A 1 31-DEC-1996;
FEATURES     Location/Qualifiers
            source
            1. 2935
BASE COUNT   697 a 856 c 810 g 572 t
ORIGIN
Query Match      88.2%; Score 19.4; DB 6; Length 2935;
Best Local Similarity 95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  CTCCTTTGGGACAGGAGGTC 22
      |||||
Db  2006 CTCCTGGGACAGGAGGTC 2026

RESULT 9
AR171867
LOCUS      AR171867          3283 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 8 from patent US 6297364.
ACCESSION  AR171867
VERSION     AR171867.1  GI:17910817
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      Chen, Y.-T., Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K.
            and Old, L.J.
TITLE       Isolated nucleic acid molecule encoding cancer associated antigen,
            the antigen itself, and uses thereof
JOURNAL     Patent: US 6297364-A 8 02-OCT-2001;
FEATURES     Location/Qualifiers
            source
            1. 3283
BASE COUNT   945 a 833 c 779 g 725 t 1 others
ORIGIN
Query Match      88.2%; Score 19.4; DB 6; Length 3283;
Best Local Similarity 95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GCTCTTTGGGACAGGAGGT 21
      |||||
Db  132 GCTCTTTGGGACAGGAGCT 152

RESULT 10
AR171865
LOCUS      AR171865          3412 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6297364.
ACCESSION  AR171865
VERSION     AR171865.1  GI:17910815
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      Chen, Y.-T., Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K.
            and Old, L.J.
TITLE       Isolated nucleic acid molecule encoding cancer associated antigen,
            the antigen itself, and uses thereof
JOURNAL     Patent: US 6297364-A 6 02-OCT-2001;
FEATURES     Location/Qualifiers
            source
            1. 3412
BASE COUNT   970 a 887 c 804 g 750 t 1 others
ORIGIN
Query Match      88.2%; Score 19.4; DB 6; Length 3412;
Best Local Similarity 95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GCTCTTTGGGACAGGAGGT 21
      |||||
Db  132 GCTCTTTGGGACAGGAGCT 152

ORIGIN
Query Match      88.2%; Score 19.4; DB 6; Length 3412;
Best Local Similarity 95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GCTCTTTGGGACAGGAGGT 21
      |||||
Db  132 GCTCTTTGGGACAGGAGCT 152

RESULT 11
BC021290
LOCUS      BC021290          3642 bp      mRNA      linear      PRI 22-JAN-2002
DEFINITION Homo sapiens, IGF-II mRNA-binding protein 2, clone MGC:29539
            IMAGE:5090334, mRNA, complete cds.
ACCESSION  BC021290
VERSION     BC021290.1  GI:18204200
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM     Homo sapiens.
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS      Strausberg, R.
TITLE       Direct Submission
JOURNAL
REFERENCE    Submitted (14-JAN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact:
            Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
            Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
            Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
            Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
            McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
            Tjongson, E.E., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A.,
            Zhang, L.-H. and Green, E.D.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 39 Row: 0 Column: 21
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 5729883.
FEATURES     Location/Qualifiers
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            /db_xref="LocusID:10644"
            /db_xref="taxon:9606"
            /clone="MGC:29539 IMAGE:5090334"
            /tissue_type="Pancreas, epithelioid carcinoma"
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            /lab_host="DH10B-R"
            /note="Vector: pOTB7"
            77. 1873
            /codon_start=1
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            /db_xref="GI:18204201"
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            PDQNWAIIRAITLQKVELHGKIMEVDYSYSKLSRSKIQIRNIPPHLQWEVLDDLLA
            QYGTVENVEQVNTDETAVNVYATREAKIWEKLSGHQFENSKISYIPEEVS
            SPSPQRAQRGDHSRSEQHAPGTSQARQIDFPLRLVPTQFVGAIGKEGLTKNI"
CDS

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TKQTSRVDIHRKENSRAEKVTHATPECTSEACRMILEIMOKADETKLAEEIPL
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APYHPTTHSGYFSSLYPHHQPPPHHSPEQIYNLPIPTQAVGAILGKGAHTK
OLARFAGASIKIAPAGSDVSRMWIITGPPFAKQGRIFGKKEENFPNKEEVK
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BASE COUNT 1077 a 919 g 849 g 797 t
ORIGIN

Query Match 88.2%; Score 19.4; DB 9; Length 3642;
Best Local Similarity 95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTCTTTGGGACAGGAAGT 21
Db 136 GCTCTTTGGGACAGGAAGT 156

RESULT 12
AF057352 3667 bp mRNA linear PRI 23-MAY-1999
LOCUS Homo sapiens hepatocellular carcinoma autoantigen (p62) mRNA,
DEFINITION complete cds.
ACCESSION AF057352
VERSION AF057352.1 GI:4883680
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3667)
Zhang J.Y., Chan, E.K., Peng, X.X. and Tan, E.M.
A novel cytoplasmic protein with RNA-binding motifs is an
autoantigen in human hepatocellular carcinoma
J. Exp. Med. 189 (7), 1101-1110 (1999)
JOURNAL 99207072
MEDLINE 10190901
PUBMED
REFERENCE 2 (bases 1 to 3667)
Zhang, J.Y., Chan, E.K.L., Peng, X.X. and Tan, E.M.
Direct Submission
Submitted (03-APR-1998) Molecular & Experimental Medicine, The
Scripps Research Institute, 10550 N. Torrey Pines Road, La Jolla,
CA 92037, USA
TITLES

FEATURES
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1..3667
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YPPQNAIRAIETLSKGLVMEVDVSVKLSRSKRIQIRNPPHLOWELDGLL
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SSPSPQAGRHDSREQHAPGGSQARQIDFPRLILVPTQFVGAIIKGEGLTIK
ITKQTSRVDIHRKENSRAEKVTHATPECTSEACRMILEIMOKADETKLAEEIP
KILAHNGLVRLIGKGRNLKIEHETGKLTISLODLSIYNPERITTVKGTVEAC
ASAEIEMKLEAFENMLAVNQANLIPGLNLSALGIFSTGLSVLSPAGPAGPAP
TOAVGAILGKGAHIKQALFAPAGASIKIAPAGSDVSRMWIITGPPFAKQGRIF
GKKEENFPNKEEVKLEAHLRVPSTAGRVIGKGTKNELNLTSAEIVPRDQTP
DENEVIRIIGHFFASQTARKIREIVQQVKQEQKYPQGVASQRSK"
BASE COUNT 1081 a 882 c 846 g 858 t
ORIGIN

Query Match 88.2%; Score 19.4; DB 9; Length 3667;
Best Local Similarity 95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAAGT 21
Db 498 GCTCTTTGGGACAGGAAGT 518

RESULT 13
AL596177 91084 bp DNA linear PRI 08-SEP-2001
LOCUS Human DNA sequence from clone RP11-325P15 on chromosome 1, complete
DEFINITION sequence.
ACCESSION AL596177
VERSION AL596177.4 GI:15552942
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 91084)
Clark, S.
Direct Submission
Submitted (08-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 11, 2001 this sequence version replaced gi:15022347.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPep; Information on the WormPep
database can be found at
http://www.sanger.ac.uk/projects/Celegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP11-325P15 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-325P15 It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-325P15 is at 1 in this sequence.
The true left end of clone RP11-337C18 is at 89085 in this
sequence. The true right end of clone RP4-704D21 is at 41034 in
this sequence.

FEATURES
source
1..91084
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-325P15"
/clone_lib="RPCI-11.2"
BASE COUNT 27074 a 19586 c 19377 g 25047 t
ORIGIN

Query Match 88.2%; Score 19.4; DB 9; Length 91084;
Best Local Similarity 95.2%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTCTTTGGGACAGGAAGT 21

```

Db 9512 GCTCTTGGGACAGAGCT 9532
|||||
RESULT 14
AC026579/c
LOCUS
DEFINITION Homo sapiens chromosome 15 clone RP11-76D16 map 15, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC026579
VERSION AC026579.2 GI:17048293
KEYWORDS HTG; HTGS PHASEO.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112259)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,E.,
Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choapel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Hagos,B., Heaford,A., Horton,L.,
Grand-Pierre,N., Grant,G., Ginde,S., Goyette,M., Graham,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazates,R., Landers,T., Lehoczy,J.,
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tefaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Vtel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 22, 2001 this sequence version replaced gi:7284066.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8359
Center clone name: 76_D_16
-----
* NOTE: This record contains 139 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1 714: contig of 714 bp in length
* 715 814: gap of 100 bp
* 815 1541: contig of 727 bp in length
* 1542 1641: gap of 100 bp

```

1642 2329: contig of 688 bp in length
 2330 2429: gap of 100 bp
 2430 3143: contig of 714 bp in length
 3144 3243: gap of 100 bp
 3244 3955: contig of 712 bp in length
 3956 4055: gap of 100 bp
 4056 4736: contig of 671 bp in length
 4737 4826: gap of 100 bp
 4827 5533: contig of 707 bp in length
 5534 5633: gap of 100 bp
 5634 6329: contig of 696 bp in length
 6330 6429: gap of 100 bp
 6430 7152: contig of 723 bp in length
 7153 7252: gap of 100 bp
 7253 7978: contig of 726 bp in length
 7979 8078: gap of 100 bp
 8079 8772: contig of 694 bp in length
 8773 8872: gap of 100 bp
 8873 9570: contig of 698 bp in length
 9571 9670: gap of 100 bp
 9671 10355: contig of 685 bp in length
 10356 10455: gap of 100 bp
 10456 11162: contig of 707 bp in length
 11163 11262: gap of 100 bp
 11263 11962: contig of 700 bp in length
 11963 12062: gap of 100 bp
 12063 12759: contig of 697 bp in length
 12760 12859: gap of 100 bp
 12860 13533: contig of 674 bp in length
 13534 13633: gap of 100 bp
 13634 14355: contig of 722 bp in length
 14356 14455: gap of 100 bp
 14456 15160: contig of 705 bp in length
 15161 15260: gap of 100 bp
 15261 15972: contig of 712 bp in length
 15973 16072: gap of 100 bp
 16073 16778: contig of 706 bp in length
 16779 16878: gap of 100 bp
 16879 17563: contig of 685 bp in length
 17564 17663: gap of 100 bp
 17664 18372: contig of 709 bp in length
 18373 18472: gap of 100 bp
 18473 19195: contig of 723 bp in length
 19196 19295: gap of 100 bp
 19296 19984: contig of 689 bp in length
 19985 20084: gap of 100 bp
 20085 20778: contig of 694 bp in length
 20779 20878: gap of 100 bp
 20879 21570: contig of 692 bp in length
 21571 21670: gap of 100 bp
 21671 22319: contig of 649 bp in length
 22320 22419: gap of 100 bp
 22420 23122: contig of 703 bp in length
 23123 23222: gap of 100 bp
 23223 23937: contig of 715 bp in length
 23938 24037: gap of 100 bp
 24038 24760: contig of 723 bp in length
 24761 24860: gap of 100 bp
 24861 25564: contig of 704 bp in length
 25565 25664: gap of 100 bp
 25665 26372: contig of 708 bp in length
 26373 26472: gap of 100 bp
 26473 27155: contig of 683 bp in length
 27156 27255: gap of 100 bp
 27256 27945: contig of 690 bp in length
 27946 28045: gap of 100 bp
 28046 28753: contig of 708 bp in length
 28754 28853: gap of 100 bp
 28854 29563: contig of 710 bp in length
 29564 29663: gap of 100 bp
 29664 30381: contig of 718 bp in length
 30382 30481: gap of 100 bp
 30482 31201: contig of 720 bp in length

Mon Apr 21 10:30:20 2003

DEFINITION Homo sapiens 12q BAC RP11-76E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

ACCESSION AC020629

VERSION AC020629.6 GI:7656675

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 142971) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Muzny, D.M., Adams, C., Bailey, M., Barberia, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Bunay, C., Bunac, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, P., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Frantz, P., Ganeh, R., Gorrell, J.H., Gorrell, L.L., Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Issat, A., Jackson, L.E., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kneitz, S., Kondejewski, N., Kong, Y., Kovar, C., Lau, S., Leal, B., Lee, E., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozano, R.J., Lu, J., Lucier, R., Marondel, I., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Merscher, S., Miller, A., Montgomery, K.T., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Osval, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Shim, C., Simon, M., Sparks, A., Stamps, A., Sugang, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wabwah, M., Watlington, S., Weinstein, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Xiang, A.M., Yang, R., Yu, W., Zhou, X., Kucherlapati, R., Nelson, D. and Gibbs, R.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 142971) Worley, K.C.

AUTHORS Direct Submission

TITLE Submitted (07-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL 3 (bases 1 to 142971) Worley, K.C.

REFERENCE Direct Submission

TITLE Submitted (27-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL 4 (bases 1 to 142971) Worley, K.C.

REFERENCE Direct Submission

TITLE Submitted (28-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL 5 (bases 1 to 142971) Worley, K.C.

REFERENCE Direct Submission

TITLE Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL On Apr 27, 2000 this sequence version replaced gi:7025656.

COMMENT INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,

31202 31301: gap of 100 bp

31302 31388: contig of 687 bp in length

31389 32088: gap of 100 bp

32089 32777: contig of 689 bp in length

32778 32877: gap of 100 bp

32878 33574: contig of 697 bp in length

33575 33674: gap of 100 bp

33675 34379: contig of 705 bp in length

34380 34479: gap of 100 bp

34480 35191: contig of 712 bp in length

35192 35291: gap of 100 bp

35292 36001: contig of 710 bp in length

36002 36101: gap of 100 bp

36102 36806: contig of 705 bp in length

36807 36906: gap of 100 bp

36907 37615: contig of 709 bp in length

37616 37715: gap of 100 bp

37716 38396: contig of 681 bp in length

38397 38496: gap of 100 bp

38497 39187: contig of 691 bp in length

39188 39287: gap of 100 bp

39288 39986: contig of 699 bp in length

39987 40086: gap of 100 bp

40087 40788: contig of 702 bp in length

40789 40888: gap of 100 bp

40889 41603: contig of 715 bp in length

41604 41703: gap of 100 bp

41704 42424: contig of 721 bp in length

42425 42524: gap of 100 bp

42525 43231: contig of 707 bp in length

43232 43331: gap of 100 bp

43332 44029: contig of 698 bp in length

44030 44129: gap of 100 bp

44130 44815: contig of 686 bp in length

44816 44915: gap of 100 bp

44916 45611: contig of 696 bp in length

45612 45711: gap of 100 bp

45712 46403: contig of 692 bp in length

46404 46503: gap of 100 bp

46504 47206: contig of 703 bp in length

47207 47306: gap of 100 bp

47307 47995: contig of 689 bp in length

47996 48095: gap of 100 bp

48096 48793: contig of 698 bp in length

48794 48893: gap of 100 bp

48894 49463: contig of 570 bp in length

49464 49563: gap of 100 bp

49564 50250: contig of 687 bp in length

50251 50350: gap of 100 bp

50351 51091: contig of 741 bp in length

51092 51191: gap of 100 bp

51192 51909: contig of 718 bp in length

51910 52009: gap of 100 bp

52010 52713: contig of 704 bp in length

52714 52813: gap of 100 bp

52814 53526: contig of 713 bp in length

53527 53626: gap of 100 bp

53627 54337: contig of 711 bp in length

54338 54437: gap of 100 bp

54438 55155: contig of 718 bp in length

Query Match 88.28; Score 19.4; DB 2; Length 112259;

Best Local Similarity 95.28; Pred. No. 33;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21

Db 77783 GCTCTTTGGGACAGGAGGT 77763

RESULT 15

AC020629

LOCUS AC020629 142971 bp DNA linear PRI 07-MAR-2002

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

```

----- Summary Statistics -----
Contig length: 142971
Phrap values in estimate: 140680
Average error rate (BCM-Phrap estimate): 0.00018703
Fraction of Phrap values less than 40: 0.0433608
Number of consensus changing edits: 31
Number of N's in consensus: 0

```

```

----- Consensus changing edits -----
Position Original+Context Edited+Context
11171 gtctctgga(n)caaaaaaaa gtctctgga(a)caaaaaaaa
12018 tatctatcg(n)ctatatctat tatctatcg(t)ctatatctat
16604 tccactctaa(n)agttccattt tccactctaa(g)agttccattt
18395 tagtaaccac(n)tacattttta tagtaaccac(t)tacattttta
21879 aaaaaaaa(n)nttaaaaca aaaaaaaa(a)aattaaaca
21880 aaaaaaaa(n)nttaaaacag aaaaaaaa(a)attaaacag
21881 aaaaaaaa(n)nttaaaacag aaaaaaaa(a)attaaacag
21906 cctaggtccc(n)ctaaatgag cctaggtccc(a)ctaaatgag
22169 accagctcg(n)ctaatggcg accagctcg(c)ctaatggcg
38915 ttacatctag(n)ctttgcaaa ttacatctag(t)ctttgcaaa
55675 acttggctc(n)aaaaaaaaa acttggctc(a)aaaaaaaaa
57558 gaccagctg(n)ccacatggt gaccagctg(a)ccacatggt
74371 gtctcgccc(n)ccgcccgcgt gtctcgccc(c)ccgcccgcgt
8021 taaatgagg(n)agaccatgg taaatgagg(a)agaccatgg
88248 gcagtggcc(n)agatcacac gcagtggcc(c)agatcacac
94121 ttgtctcga(n)gctctctgc ttgtctcga(t)gctctctgc
95230 gtcacatgt(n)nnntgttca ccatgtctc(n)nnntgttca
95231 ccatgtctc(n)nnntgttca ccatgtctc(c)nnntgttca
95232 atgtgtnnn(n)ttgttcaac atgtgtnnn(a)ttgttcaac
104931 tttttttag(n)acagacagg tttttttag(t)acagacagg
118168 gccacgtgt(n)ccaaagtgt gccacgtgt(c)ccaaagtgt
120974 catctcaaa(n)anangaac catctcaaa(a)anangaac
120976 tctcaaaa(n)anangaact tctcaaaa(a)anangaact
120978 tcaaaaana(n)angaacttt tcaaaaana(a)angaacttt
120980 aaaaana(n)gaactcttc aaaaana(a)gaactcttc
139505 ccagccatgg(n)ggngggacc ccagccatgg(t)ggngggacc
139508 gccatgngg(n)ggngggacc gccatgngg(t)ggngggacc
139698 attaccatta(n)aatatgat attaccatta(t)aatatgat
140104 accgtgccca(n)gagataga accgtgccca(g)gagataga
140149 tggacaact(n)gataccaca tggacaact(g)gataccaca

```

----- Distribution of Quality < 40 Bases -----

```

1000|
900|

```

```

#
bases
800
700
600
500
400
300
200
100
0

```

```

Version: 1.01 qxfo.
FEATURES
Source
1. 142971 Location/Qualifiers
/db_xref="taxon:9606"
/chromosomes="12"
/clone="RP11-76E16"
147. 236
/rpt_family="A-rich"
258. 378
/rpt_family="AluJb"
complement(537. 840)
/rpt_family="AluX"
complement(1722. 2137)
/rpt_family="nigger2a"
complement(3161. 3584)
/rpt_family="MSTD"
3228. 3502
/standard_name="G05956"
/db_xref="dbSTS:11453"
3347. 3490
/standard_name="Cda0yb04"
/db_xref="GDB:446196"
3585. 3735
/note="Region similar to Hs#S936143 aj27d02.s1 Homo sapiens cDNA: AA789222"
3885. 3910
/rpt_family="(TA)n"
complement(3917. 4030)
/rpt_family="AluJb"
complement(4544. 4681)
/rpt_family="MIR"
5145. 5510
/note="Region similar to Hs#S953417 oa06g05.s1 Homo sapiens cDNA: AA765439"
5553. 5859
/note="Region similar to Hs#S1195593 qt69f10.x1 Homo sapiens cDNA: A1285403"

```

```

Query Match 88.2%; Score 19.4; DB 9; Length 142971;
Best Local Similarity 95.2%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 GCTCTTTGGGACAGGAGCT 21

Db 133084 GCTCTTTGGGACAGGAGCT 133104

Search completed: April 18, 2003, 06:27:37
Job time : 414 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:12:35 / Search time 98 Seconds
(without alignments)
505.551 Million cell updates/sec

Title: US-09-270-437D-13

Perfect score: 22

Sequence: 1 gctcttggggacaggagtc 22

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N_Geneseq_101002.*

- 1: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
- 2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
- 3: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
- 4: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
- 5: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
- 6: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
- 7: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
- 8: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
- 9: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
- 10: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
- 11: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
- 12: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
- 13: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
- 14: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
- 15: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
- 16: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
- 17: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
- 18: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
- 19: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
- 21: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	21	AAZ36159
2	19.4	88.2	364	21	AAZ36159
3	19.4	88.2	2010	23	AAZ36159
4	19.4	88.2	2335	17	AAZ36159
5	19.4	88.2	2335	17	AAZ36159
6	19.4	88.2	2335	18	AAZ36159
7	19.4	88.2	2335	18	AAZ36159
8	19.4	88.2	2335	20	AAZ36159
9	19.4	88.2	3283	21	AAZ36159

10	19.4	88.2	3412	21	AAZ36152
11	19.4	88.2	3667	23	AAZ36152
12	19.4	88.2	3694	22	AAZ36150
13	17.8	80.9	1212	19	AAZ36150
14	17.8	80.9	11849	20	AAZ36150
15	17.4	79.1	3036	22	AAZ36150
16	17.2	78.2	429	24	AAZ36150
17	17.2	78.2	778	21	AAZ36150
18	17.2	78.2	801	22	AAZ36150
19	17.2	78.2	4985	20	AAZ36150
20	17.2	78.2	5526	23	AAZ36150
21	17.2	78.2	5778	22	AAZ36150
22	17.2	78.2	5804	22	AAZ36150
23	17.2	78.2	6042	23	AAZ36150
24	16.8	76.4	401	22	AAZ36150
25	16.8	76.4	401	22	AAZ36150
26	16.8	76.4	1442	21	AAZ36150
27	16.8	76.4	4159	23	AAZ36150
28	16.8	76.4	4394	13	AAZ36150
29	16.8	76.4	5364	22	AAZ36150
30	16.8	76.4	5364	22	AAZ36150
31	16.4	74.5	544	22	AAZ36150
32	16.4	74.5	927	19	AAZ36150
33	16.4	74.5	952	22	AAZ36150
34	16.4	74.5	952	22	AAZ36150
35	16.4	74.5	1452	21	AAZ36150
36	16.4	74.5	1452	21	AAZ36150
37	16.4	74.5	1452	21	AAZ36150
38	16.4	74.5	1452	24	AAZ36150
39	16.4	74.5	1487	21	AAZ36150
40	16.4	74.5	1599	24	AAZ36150
41	16.4	74.5	1680	18	AAZ36150
42	16.4	74.5	1680	19	AAZ36150
43	16.4	74.5	1680	19	AAZ36150
44	16.4	74.5	1680	20	AAZ36150
45	16.4	74.5	1680	20	AAZ36150

ALIGNMENTS

RESULT 1
AAZ36159
ID AAZ36159 standard; DNA; 22 BP.
XX AAZ36159;
AC AAZ36159;
XX AAZ36159;
DT 11-FEB-2000 (first entry)
DE PCR primer for DNA encoding cancer associated antigen KOC-3.
XX Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss.
XX Synthetic.
OS Homo sapiens.
XX WO9954738-A1.
XX 28-OCT-1999.
XX 16-MAR-1999; 99WO-US05766.
XX 17-APR-1998; 98US-0061709.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;
XX WPI; 2000-013284/01.
XX Nucleotides representing cancer-associated genes, used to develop
PT products for the diagnosis, monitoring and treatment of cancers -
XX

Query Match	88.2%;	Score 19.4;	DB 17;	Length 2935;
Best Local Similarity	95.2%;	Pred. No. 14;		

RESULT 6

us-09-270-437d-13.rng

Mon Apr 21 10:30:22 2003

AAT59199
ID AAT59199 standard; cDNA; 2935 BP.
AC AAT59199;
XX
XX
XX 20-MAY-1997 (first entry)
DT
XX
XX Ca-independent phospholipase A2/B gene.
DE
XX Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
KW chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
KW heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;
KW CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade; ds.
XX
XX Chinese hamster ovary cells.
OS
XX
XX
XX Key Location/Qualifiers
FH 96..2354
FT CDS /*tag= a
FT /product= ca-independent phospholipase A2/B
XX
XX US5589170-A.
XX
XX 31-DEC-1996.
XX
XX 27-JUL-1994; 94US-0281193.
XX
XX 27-JUL-1994; 94US-0281193.
XX
XX 14-APR-1995; 95US-0422106.
XX
XX (GEMY) GENETICS INST INC.
XX
XX Jones S, Tang J;
PI WPI; 1997-076789/07.
DR P-PSDB; AAW13163.
DR
XX Compn. comprising calcium-independent phospholipase enzyme - for
PT screening for anti-inflammatory agents
PT
XX Claim 5; Column 15-22; 24pp; English.
XX
XX This is the nucleotide sequence encoding the Ca-independent
CC phospholipase A2/B from Chinese hamster ovary cells. The protein was
CC isolated from these cells by conventional chromatographic methods e.g.
CC DEAE anion exchange, hydrophobic interaction, heparin Toyopearl and Mono
CC P 5/20 chromatofocusing chromatography. The purified protein has mol.
CC wt. of 86 kD and an optimum pH 6. The protein was used for amino acid
CC sequencing from which pools of degenerate probes were synthesised. The
CC probes were used to screen a CHO cell cDNA library in lambda ZAPII
CC vector. Of 40000 recombinant phages screened, 12 positive plaques were
CC isolated. One of these, designated clone 9, contained this sequence.
CC The phospholipase gene can be inserted into eukaryotic vectors for
CC expression in COS or CHO cells. The protein, or peptides derived from it
CC e.g. AAW13164-76, can be used to identify phospholipase inhibitors that
CC can be used as anti-inflammatory agents, esp. against components of the
CC arachidonic acid cascade.
XX
XX Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 other;
SQ
Query Match 88.2%; Score 19.4; DB 18; Length 2935;
Best Local Similarity 95.2%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CTCTTTGGGACAGGAGGTC 22
Db 2006 CTCTCTGGGACAGGAGGTC 2026
RESULT 7
AAT68827
ID AAT68827 standard; cDNA; 2935 BP.
XX

AAT68827;
AC
XX 07-AUG-1997 (first entry)
XX
XX Hamster cytosolic phospholipase A2/B cDNA.
DE
XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
KW inflammation; inhibitor; antiinflammatory; CHO; ds.
XX
XX Cricetus sp.
OS
XX Location/Qualifiers
FH 96..2354
FT CDS /*tag= a
FT
XX WO9717448-A2.
XX
XX 15-MAY-1997.
XX
XX 07-NOV-1996; 96WO-US17794.
XX
XX 08-NOV-1995; 95US-0555568.
XX
XX (GEMY) GENETICS INST INC.
XX
XX Jones S, Tang J;
PI WPI; 1997-281037/25.
DR P-PSDB; AAW17849.
DR
XX Calcium independent phospholipase A2/B - used to reduce inflammation
PT in a mammalian subject
PT
XX Example 4; Page 33-36; 74pp; English.
XX
XX A cDNA clone (AAT68827), deposited as ATCC 69669, codes for a
CC cytosolic phospholipase A2/B (sPLA2/B) that is thought to
CC be involved in the arachidonic acid cascade. It was obtd. by
CC screening a CHO-DUX cDNA library with probes based on isolated
CC peptides of the enzyme. Recombinant sPLA2/B was expressed in
CC COS and CHO cells. Probes based on the hamster sPLA2/B clone
CC were used to identify human sPLA2/B partial cDNA clones (see also
CC AAT68823-26).
XX
XX Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 other;
SQ
Query Match 88.2%; Score 19.4; DB 18; Length 2935;
Best Local Similarity 95.2%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CTCTTTGGGACAGGAGGTC 22
Db 2006 CTCTCTGGGACAGGAGGTC 2026
RESULT 8
AAV64840
ID AAV64840 standard; cDNA; 2935 BP.
XX
XX AAV64840;
XX
XX 02-FEB-1999 (first entry)
XX
XX Chinese hamster calcium independent cPLA2/B cDNA.
DE
XX Calcium independent; cytosolic phospholipase A2/B; screening;
KW anti-inflammatory; arachidonic acid cascade; Chinese hamster; ds.
XX
XX Cricetus griseus.
OS
XX
XX Key Location/Qualifiers
FH 96..2354
FT CDS /*tag= a
FT

FT XX US5840511-A. /product= "calcium independent cPLA2/B"

PN XX 24-NOV-1998.

PD XX 23-OCT-1996; 96US-0735716.

PF XX 27-JUL-1994; 94US-0281193.

PR XX 14-APR-1995; 95US-0422106.

PS XX 23-OCT-1996; 96US-0735716.

PT (GEM) GENETICS INST INC.

PI Jones S, Tang J;

XX WPI; 1999-034032/03.

DR P-PSDB; AAW81825.

XX Screening assay for phospholipase inhibitors - using specified

PT phospholipase polypeptide

XX Claim 1b(1); Column 15-22; 24pp; English.

PS This sequence encodes a novel calcium independent cytosolic phospholipase

CC A2/B enzyme isolated from chinese hamster ovary cells. This protein can

CC be used for screening unknown compounds for anti-inflammatory activity

CC mediated by the arachidonic acid cascade.

XX Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 other;

SQ

Query Match 88.2%; Score 19.4; DB 20; Length 2935;

Best Local Similarity 95.2%; Pred. No. 14;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCTTTGGGACAGGAGTC 22

DB 2006 CTCTTTGGGACAGGAGTC 2026

RESULT 9

AAZ36154

ID AAZ36154 standard; DNA; 3283 BP.

XX AAZ36154;

AC 11-FEB-2000 (first entry)

XX An alternative form of DNA encoding cancer associated antigen KOC-3.

DE Cancer associated antigen; KOC-3; cancer; vaccine; CT7; ss.

XX Homo sapiens.

OS WO9954738-A1.

PN 28-OCT-1999.

XX 16-MAR-1999; 99WO-US05766.

PF 17-APR-1998; 98US-0061709.

XX (LUDW-) LUDWIG INST CANCER RES.

PA Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;

PI WPI; 2000-013284/01.

XX Nucleotides representing cancer-associated genes, used to develop

PT products for the diagnosis, monitoring and treatment of cancers -

XX Claim 55; Page 42-43; 44pp; English.

CC The present sequence represents an alternative form of a cancer

CC associated antigen gene designated KOC-3. The specification also

CC describes a cancer associated antigen designated CT7. The CT7

CC polynucleotide was isolated from SK-MEL-37 melanoma cells. The

CC polypeptide has some homology with MAGE-10, limited to about 210 carboxy

CC terminal amino acids. The amino terminal of the protein has a repetitive

CC pattern, with repeats rich in serine, proline, glutamine and leucine,

CC and an almost invariable core of the peptide given in AA43877. The CT7

CC polypeptide can be processed to peptides which provoke lysis by

CC cytolytic T cells. The polynucleotides and polypeptides can be used for

CC treating a cancerous condition and screening for or diagnosing cancerous

CC conditions. The cancer associated antigens can be used as an immunogenic

CC or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or

CC granulocyte macrophage-colony stimulating factor (GM-CSF).

XX

SQ Sequence 3283 BP; 945 A; 833 C; 779 G; 725 T; 1 other;

Query Match 88.2%; Score 19.4; DB 21; Length 3283;

Best Local Similarity 95.2%; Pred. No. 14;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGT 21

DB 132 GCTCTTTGGGACAGGAGT 152

RESULT 10

AAZ36152

ID AAZ36152 standard; DNA; 3412 BP.

XX AAZ36152;

AC 11-FEB-2000 (first entry)

XX DNA encoding cancer associated antigen KOC-3.

DE Cancer associated antigen; KOC-3; cancer; vaccine; CT7; ss.

XX Homo sapiens.

OS WO9954738-A1.

PN 28-OCT-1999.

XX 16-MAR-1999; 99WO-US05766.

PF 17-APR-1998; 98US-0061709.

XX (LUDW-) LUDWIG INST CANCER RES.

PA Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;

PI WPI; 2000-013284/01.

XX Nucleotides representing cancer-associated genes, used to develop

PT products for the diagnosis, monitoring and treatment of cancers -

XX Claim 55; Page 41; 44pp; English.

CC The present sequence represents a cancer associated antigen gene

CC designated KOC-3. The specification also describes a cancer associated

CC antigen designated CT7. The CT7 polynucleotide was isolated from

CC SK-MEL-37 melanoma cells. The polypeptide has some homology with

CC MAGE-10, limited to about 210 carboxy terminal amino acids. The amino

CC terminal of the protein has a repetitive pattern, with repeats rich in

CC serine, proline, glutamine and leucine, and an almost invariable core of

CC the peptide given in AA43877. The CT7 polypeptide can be processed to

CC peptides which provoke lysis by cytolytic T cells. The polynucleotides

CC and polypeptides can be used for treating a cancerous condition and

CC screening for or diagnosing cancerous conditions. The cancer associated

CC antigens can be used as an immunogenic or vaccine composition with an

CC adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony

CC stimulating factor (GM-CSF).

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XX Sequence 3412 BP; 970 A; 887 C; 804 G; 750 T; 1 other;

SQ Query Match 88.2%; Score 19.4; DB 21; Length 3412;
Best Local Similarity 95.2%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21
|||||
Db 132 GCTCTTTGGGACAGGAGGT 152

RESULT 11
AAS70982
ID AAS70982 standard; cDNA; 3667 BP.

XX AC AAS70982;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #6786.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG06795.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

XX PS Claim 1; SEQ ID No 6786; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 3667 BP; 1081 A; 882 C; 846 G; 858 T; 0 other;

Query Match 88.2%; Score 19.4; DB 23; Length 3667;
Best Local Similarity 95.2%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21
|||||
Db 498 GCTCTTTGGGACAGGAGGT 518

RESULT 12
AAS26150
ID AAS26150 standard; cDNA; 3694 BP.

XX AC AAS26150;

XX DT 07-NOV-2001 (first entry)

XX DE Human cDNA encoding a novel secreted protein, Seq ID 329.

XX KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;
KW cystostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW vulnery; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.

XX OS Homo sapiens.

XX PN WO200155322-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01341.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 07-JUL-2000; 2000US-0216880.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 11-JUL-2000; 2000US-0217496.

XX PR 26-JUL-2000; 2000US-0218290.

XX PR 26-JUL-2000; 2000US-0220963.

XX PR 26-JUL-2000; 2000US-0220964.

XX PR 14-AUG-2000; 2000US-0224518.

XX PR 14-AUG-2000; 2000US-0224519.

XX PR 14-AUG-2000; 2000US-0225213.

XX PR 14-AUG-2000; 2000US-0225214.

XX PR 14-AUG-2000; 2000US-0225266.

XX PR 14-AUG-2000; 2000US-0225267.

XX PR 14-AUG-2000; 2000US-0225268.

XX PR 14-AUG-2000; 2000US-0225270.

XX PR 14-AUG-2000; 2000US-0225447.

XX PR 14-AUG-2000; 2000US-0225757.

XX PR 14-AUG-2000; 2000US-0225758.

XX PR 14-AUG-2000; 2000US-0225759.

XX PR 18-AUG-2000; 2000US-0226279.

XX PR 22-AUG-2000; 2000US-0226681.

XX PR 22-AUG-2000; 2000US-0226868.

XX PR 22-AUG-2000; 2000US-0227182.

XX PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 06-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-023113.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0232081.
 PR 14-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 25-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 26-SEP-2000; 2000US-0234998.
 PR 27-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246509.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.

PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 05-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-488783/53.
 P-PSDB; AAU16163.

New nucleic acid molecules encoding 461 human secreted proteins for
 diagnosing, preventing, treating or ameliorating medical conditions and
 used as food additives or preservatives -
 Claim 1; SEQ ID No 329; 980pp; English.

The invention relates to isolated nucleic acid molecules and their
 encoded secreted proteins. The nucleic acids and proteins are used to
 prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 rabbits, goats, horses, cats, dogs, chickens or sheep. They
 are also used in diagnosing a pathological condition or susceptibility
 to a pathological condition. Antibodies to the proteins can also
 be used in alleviating symptoms associated with the disorders and in
 diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
 immunosorbant assays (ELISA). Disorders which are diagnosed or treated
 include autoimmune diseases e.g. rheumatoid arthritis,
 hyperproliferative disorders e.g. neoplasms of the breast or liver,
 cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
 Alzheimer's disease, infections caused by bacteria, viruses and fungi
 and ocular disorders e.g. corneal infection, and many other
 disorders listed in the specification. The polypeptides can also
 be used to aid wound healing and epithelial cell proliferation, to
 prevent skin aging due to sunburn, to maintain organs before
 transplantation, for supporting cell culture of primary tissues, to
 regenerate tissues and in chemotaxis. The polypeptides can also be used
 as a food additive or preservative to increase or decrease storage
 capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 minerals, cofactors and other nutritional components. The present
 sequence encodes a novel secreted protein of this invention.

Query Match 88.2%; Score 19.4; DB 22; Length 3694;
 Best Local Similarity 95.2%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGGACAGGAGGT 21
 |||||

XX	AA233905;
AC	
CC	25-JAN-2000 (first entry)
DT	
DE	Human LOBO homologue genomic DNA fragment 7.
KW	LOBO; long bones; bone development; bone extension; skull; osteopathic;
KW	diagnostic; pharmaceutical; gene therapy; transgenic animal; disease;
KW	spondyloepiphyseal dysplasia; achondroplasia; human; ds.
OS	Homo sapiens.
PN	WO9950284-A2.
PD	07-OCT-1999.
PF	26-MAR-1999; 99WO-EP02055.
PR	27-MAR-1998; 98DE-1013799.
PP	(ROSE/) ROSENTHAL A.
PI	Rosenthal A, Rump A, Hess J, Aigner T, Wirth T;
DR	WPI; 1999-601320/51.
PT	Nucleic acids encoding proteins which influence bone development,
PT	useful for treating and studying bone disorders -
PS	Example 3; Page 384-391; 391pp; German.
CC	This invention describes novel nucleic acids (I; designated LOBO (long
CC	bones)) encoding proteins influencing bone development in mammals. The
CC	proteins of the invention reduce and/or inactivate bone extension (i.e.
CC	development), with exception of the skull and have osteopathic activit
CC	The nucleic acid molecules, proteins and antibodies can be used in
CC	diagnostic or pharmaceutical compounds e.g. for gene therapy. The meth
CC	and nucleic acid molecules, etc. are useful for production of transgen
CC	animals, especially a transgenic mouse for the study of diseases
CC	associated with bone development, e.g. spondyloepiphyseal dysplasia and
CC	achondroplasia. This sequence encodes a human LOBO protein described
CC	in the method of the invention.
SQ	Sequence 11849 BP; 2693 A; 3311 C; 3343 G; 2502 T; 0 other;
Query Match 80.9%; Score 17.8; DB 20; Length 11849;	
Best Local Similarity 90.5%; Pred. NO. 93;	
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps	
QY	1 GCTCTTTGGGACAGGAGGT 21
Db	7320 GCTCTTTGGGTCGGAAGAT 7300
RESULT 15	
AAH34291/c	
ID	AAH34291 standard; cDNA; 3036 BP.
XX	
AC	AAH34291;
XX	
DT	03-SEP-2001 (first entry)
XX	
DE	Human colon cancer antigen encoding cDNA SEQ ID NO:1373.
XX	
KW	Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW	colorectal carcinoma; ss.
XX	
OS	Homo sapiens.
XX	
FN	WO200122920-A2.
PN	
PD	05-APR-2001.

XX 28-SEP-2000; 2000WO-US26524.
 XX 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX
 DR WPI; 2001-235357/24.
 DR P-PSDB; AAG74886.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 1; Page 3084-3085; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAG77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 3036 BP; 961 A; 603 C; 633 G; 830 T; 9 other;

Query Match 79.1%; Score 17.4; DB 22; Length 3036;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GCTCTTTGGGACAGGAG 19
 |||
 Db 2881 GCCTTTGGGACAGGAG 2863

Search completed: April 18, 2003, 05:45:32
 Job time : 104 secs

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:53:41 ; Search time 21.5 Seconds
(without alignments)
313.809 Million cell updates/sec

Title: US-09-270-437D-13

Perfect score: 22
Sequence: 1 gctcttggggacaggaggtc 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	88.2	2935	1	US-08-281-193-1
2	19.4	88.2	2935	1	US-08-422-106-1
3	19.4	88.2	2935	2	US-08-735-716-1
4	19.4	88.2	2935	2	US-08-555-568B-1
5	19.4	88.2	2935	4	US-09-519-223-1
6	19.4	88.2	2935	5	PCT-US95-08069-1
7	19.4	88.2	3283	4	US-09-061-709-8
8	19.4	88.2	3412	4	US-09-061-709-6
9	17.2	78.2	4985	4	US-09-473-717-1
10	17.2	78.2	5515	4	US-09-398-193-98
11	16.4	74.5	927	4	US-08-928-862-2
12	16.4	74.5	1680	1	US-08-140-729A-2
13	16.4	74.5	1680	1	US-08-546-666-2
14	16.4	74.5	1680	2	US-08-316-745-2
15	16.4	74.5	1680	2	US-09-042-929-2
16	16.4	74.5	1680	2	US-08-546-661-2
17	16.4	74.5	1680	2	US-09-042-960-2
18	16.4	74.5	1680	3	US-09-198-650-2
19	16.4	74.5	1680	3	US-09-042-913-2
20	16.4	74.5	1680	3	US-09-042-937-2
21	16.2	73.6	1277	4	US-09-042-709A-2
22	16.2	73.6	1277	4	US-08-555-568B-18
23	16.2	73.6	1277	4	US-09-519-223-18
24	16.2	73.6	1707	1	US-08-790-309-1
25	16.2	73.6	1707	4	US-09-250-585A-1
26	16.2	73.6	1710	2	US-08-912-794-1
27	16.2	73.6	2109	2	US-08-555-568B-20

28	16.2	73.6	2109	4	US-09-519-223-20	Sequence 20, Appl
29	16.2	73.6	2112	2	US-08-555-568B-22	Sequence 22, Appl
30	16.2	73.6	2112	4	US-09-519-223-22	Sequence 22, Appl
31	16.2	73.6	3240	4	US-08-851-896-10	Sequence 10, Appl
32	16.2	73.6	70000	4	US-09-851-896-3	Sequence 3, Appl
C 33	16	72.7	1641	3	US-08-705-771-9	Sequence 9, Appl
C 34	16	72.7	1662	1	US-08-336-408B-5	Sequence 5, Appl
C 35	16	72.7	1662	5	PCT-US91-00399-5	Sequence 5, Appl
C 36	15.8	71.8	401	4	US-09-221-298-40	Sequence 40, Appl
C 37	15.8	71.8	446	4	US-09-641-638-500	Sequence 500, Appl
C 38	15.8	71.8	459	4	US-09-443-041A-13	Sequence 13, Appl
C 39	15.8	71.8	658	4	US-09-385-982-94	Sequence 94, Appl
C 40	15.8	71.8	1447	4	US-09-443-041A-27	Sequence 27, Appl
C 41	15.8	71.8	2002	2	US-08-715-202A-3	Sequence 3, Appl
C 42	15.8	71.8	2002	4	US-09-328-775-3	Sequence 3, Appl
C 43	15.8	71.8	3770	4	US-09-221-017B-807	Sequence 807, Appl
C 44	15.6	70.9	2349	2	US-08-974-546-2	Sequence 2, Appl
C 45	15.6	70.9	3490	2	US-08-841-483-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-281-193-1
; Sequence 1, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 96..2352
US-08-281-193-1

Query Match 88.2%; Score 19.4; DB 1; Length 2935;
Best Local Similarity 95.3%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CTCCTTGGGGACAGGAGGTC 22
Db 2006 CTCCTTGGGGACAGGAGGTC 2026

RESULT 2
US-08-422-106-1
; Sequence 1, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,106
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 96..2352
US-08-422-106-1

Query Match 88.2%; Score 19.4; DB 1; Length 2935;
Best Local Similarity 95.2%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCTTTGGGACAGGAGGTC 22
DB 2006 CTCTCTGGGGACAGGAGGTC 2026

RESULT 3
US-08-735-716-1
Sequence 1, Application US/08735716
Patent No. 5840511
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,716
FILING DATE: 23-OCT-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 96..2352
US-08-735-716-1

Query Match 88.2%; Score 19.4; DB 2; Length 2935;
Best Local Similarity 95.2%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCTTTGGGACAGGAGGTC 22
DB 2006 CTCTCTGGGGACAGGAGGTC 2026

RESULT 4
US-08-555-568B-1
Sequence 1, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 96..2352
US-08-555-568B-1

Query Match 88.2%; Score 19.4; DB 2; Length 2935;
Best Local Similarity 95.2%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCTTTGGGACAGGAGGTC 22
DB 2006 CTCTCTGGGGACAGGAGGTC 2026

RESULT 5
US-09-519-223-1
Sequence 1, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge

Query Match 88.2%; Score 19.4; DB 2; Length 2935;
Best Local Similarity 95.2%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LOCATION:
PCT-US95-08069-1

Qy 1 GCTCTTTGGGGACAGGAAGGT 21
Db 132 GCTCTTTGGGGACAGGAAGCT 152

```

RESULT 9
US-09-473-717-1/C
/ Sequence 1, Application US/09473717
/ Patent No. 6372475
/ GENERAL INFORMATION:
/ APPLICANT: Storm, Daniel R.
/ APPLICANT: Hacker, Beth
/ APPLICANT: Tomlinson, James E.
/ APPLICANT: COR Therapeutics, Inc.
/ APPLICANT: University of Washington
/ TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
/ TITLE OF INVENTION: CYCLASE
/ FILE REFERENCE: 44481-5029-01-US
/ CURRENT APPLICATION NUMBER: US/09/473,717
/ CURRENT FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: PCT/US98/13541
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/098,559
/ PRIOR FILING DATE: 1997-07-01
/ PRIOR APPLICATION NUMBER: 08/886,440
/ PRIOR FILING DATE: 1997-07-01
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 4985
/ TYPE: DNA
/ ORGANISM: human type IX adenylyl cyclase
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (17)..(3898)
/ US-09-473-717-1

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Query Match	78.2%;	Score 17.2;	DB 4;	Length 4985;
Best Local Similarity	86.4%;	Pred. No. 18;		
		Mismatches	3.	Indels 0;
		Gaps	0;	

2y
1 GCTCTTTGGGACAGGAAGTTC 22

b
3751 GCACCTTTGGGTACAGGTAGTTC 3730

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RESULT 10
US-09-398-193-98/C
; Sequence 98, Application US/09398193
;
; GENERAL INFORMATION:
; PATENT NO. 6197581
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylyate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 5515
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (539)..(4600)
;
; US-09-398-193-98

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Query Match	78.2%;	Score 17.2;	DB 4;	Length 5515;
Best Local Similarity	86.4%;	Prod. No. 18;		
Matches 19:	Conservative	0;	Mismatches	3;
			Indels	0;
			Gaps	0;

QY . 1 GCTCTTTGGGACAGGAAGGTC 22

4273 GCACTTTGGGTACAGGTAGGTC 4252

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RESULT 11
US-08-928-862-2/c
; Sequence 2, Application US/08928862
; Patent No. 6309877
; GENERAL INFORMATION:
; APPLICANT: Chau, Raymond M. W.
; TITLE OF INVENTION: Isolation and Use of Motoneuronotrophic Factors
; FILE REFERENCE: 12592-2
; CURRENT APPLICATION NUMBER: US/08/928,862
; CURRENT FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-928-862-2

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Query Match	74.5%;	Score 16.4;	DB 4;	Length 927;
Best Local Similarity	94.4%;	Pred. No. 32;		
Matches 17; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;

Qy 4 CTTTGGGGACAGGAAGGT 21
db 200 CTGTGGGGACAGGAAGGT 183

RESULT 12
US-08-140-729A-2/c
Sequence 2, Application US/08140729A
Patent No. 5658782
GENERAL INFORMATION:
APPLICANT: Amara, Susan G
APPLICANT: Arriza, Jeffrey L
TITLE OF INVENTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

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FEATURE:
NAME/KEY: CDS
LOCATION: 31..1626
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1626..1680
US-08-140-729A-2

Query Match 74.5%; Score 16.4; DB 1; Length 1680;
Best Local Similarity 94.4%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCCTTTGGGACAGGAG 19
|||||
DB 528 CTCCTTTGGGACAGGAG 511

RESULT 13
US-08-546-666-2/c
Sequence 2, Application US/08546666
Patent No. 5776774
GENERAL INFORMATION:
APPLICANT: Amara, Susan G
TITLE OF INVENTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546.666
FILING DATE: 20 OCT 1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/140,729
FILING DATE: 20 OCT 1993

ATTORNEY/AGENT INFORMATION:
NAME: No. 5776774nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,509
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: 5'UTR
LOCATION: 1..30
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1626
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1626..1680
US-08-546-666-2

Query Match 74.5%; Score 16.4; DB 1; Length 1680;
Best Local Similarity 94.4%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CTCCTTTGGGACAGGAG 19
|||||
DB 528 CTCCTTTGGGACAGGAG 511

RESULT 14
US-08-916-745-2/c
Sequence 2, Application US/08916745
Patent No. 5840516
GENERAL INFORMATION:
APPLICANT: Amara, Susan G
TITLE OF INVENTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916.745
FILING DATE: 19-AUG-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/140,729
FILING DATE: 20-OCT-1993
ATTORNEY/AGENT INFORMATION:

NAME: No. 5840516nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,509
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: 5'UTR
LOCATION: 1..30
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1626
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1626..1680
US-08-916-745-2

Query Match 74.5%; Score 16.4; DB 2; Length 1680;
Best Local Similarity 94.4%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCCTTTGGGACAGGAG 19
|||||
DB 528 CTCCTTTGGGACAGGAG 511

RESULT 15
US-09-042-929-2/c
Sequence 2, Application US/09042929

us-09-270-437d-13.rnd

Mon Apr 21 10:30:23 2003

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; Patent No. 5919628
; GENERAL INFORMATION:
; APPLICANT: Amara, Susan G
; APPLICANT: Arriza, Jeffrey L
; TITLE OF INVENTION: Amino Acid Transporters and Uses
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,929
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,729
; FILING DATE: 20 OCT 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5919628nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,509
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..30
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1626
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1626..1680
; US-09-042-929-2

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Query Match      74.5%; Score 16.4; DB 2; Length 1680;
Best Local Similarity 94.4%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy  2 CTCTTTGGGGACAGGAG 19
Db  528 CTCTTTGGGGACAGGAG 511

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Search completed: April 18, 2003, 07:34:33
Job time : 24.5 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:31 ; Search time 91.3333 Seconds
(without alignments)
241.975 Million cell updates/sec

Title: US-09-270-437D-13

Perfect score: 22

Sequence: 1 gctcttggggacaggagtc 22

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Searched: 639749 seqs, 502280978 residues

Total number of hits satisfying chosen parameters: 1279498

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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- 2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq:
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- 12: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq:
- 13: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq:
- 14: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	88.2	2935	10 US-09-927-180-1	Sequence 1, Appli
2	19.4	88.2	3283	10 US-09-899-651-8	Sequence 8, Appli
3	19.4	88.2	3412	10 US-09-899-651-6	Sequence 6, Appli
4	19.4	88.2	3694	10 US-09-764-864-329	Sequence 329, App
5	17.2	78.2	4985	12 US-10-071-223-1	Sequence 1, Appli
6	17.2	78.2	5515	10 US-09-751-100B-98	Sequence 98, Appli
7	16.8	76.4	401	9 US-09-946-807-702	Sequence 702, App
8	16.8	76.4	401	10 US-09-795-668-702	Sequence 702, App
9	16.8	76.4	401	10 US-09-795-686-702	Sequence 702, App
10	16.8	76.4	80959	9 US-09-858-546-3	Sequence 3, Appli
11	16.4	74.5	15531	9 US-10-125-540-600	Sequence 600, App
12	16.4	74.5	15531	9 US-09-764-870-600	Sequence 600, App
13	16.4	74.5	659138	9 US-09-771-208-20	Sequence 20, Appl
14	16.2	73.6	256	10 US-09-878-574-5931	Sequence 5931, Ap
15	16.2	73.6	275	10 US-09-878-574-5931	Sequence 9673, Ap
16	16.2	73.6	694	10 US-09-878-574-4815	Sequence 4815, Ap
17	16.2	73.6	1277	10 US-09-927-180-18	Sequence 18, Appl
18	16.2	73.6	2109	10 US-09-927-180-20	Sequence 20, Appl
19	16.2	73.6	2112	10 US-09-927-180-22	Sequence 22, Appl

20	16.2	73.6	3231	10 US-09-864-864-306	Sequence 306, App
21	16.2	73.6	24707	9 US-10-274-968-3	Sequence 3, Appli
22	16.2	73.6	24707	10 US-09-740-027-3	Sequence 1159, Ap
23	16	72.7	361	9 US-09-736-457-1159	Sequence 1159, Ap
24	16	72.7	361	9 US-09-902-941-1159	Sequence 1159, Ap
25	16	72.7	361	9 US-09-849-626-1159	Sequence 1159, Ap
26	16	72.7	361	9 US-10-017-754-1159	Sequence 1159, Ap
27	16	72.7	437	10 US-09-917-800A-392	Sequence 392, App
28	16	72.7	669	10 US-09-917-800A-486	Sequence 486, App
29	16	72.7	1594	10 US-09-964-824A-559	Sequence 559, App
30	15.8	71.8	339	9 US-09-803-719-978	Sequence 978, App
31	15.8	71.8	401	9 US-10-025-380-40	Sequence 40, Appl
32	15.8	71.8	401	10 US-09-922-217-40	Sequence 40, Appl
33	15.8	71.8	401	10 US-09-833-263-40	Sequence 40, Appl
34	15.8	71.8	409	10 US-09-960-352-9154	Sequence 9154, Ap
35	15.8	71.8	412	10 US-09-960-352-14119	Sequence 14119, A
36	15.8	71.8	449	10 US-09-998-598-2037	Sequence 2037, Ap
37	15.8	71.8	527	10 US-09-920-300A-1339	Sequence 1339, Ap
38	15.8	71.8	527	12 US-10-033-528-1339	Sequence 1339, Ap
39	15.8	71.8	689	10 US-09-917-800A-1159	Sequence 1159, Ap
40	15.8	71.8	787	9 US-10-025-380-132	Sequence 132, App
41	15.8	71.8	787	10 US-09-922-217-132	Sequence 132, App
42	15.8	71.8	787	10 US-09-833-263-132	Sequence 132, App
43	15.8	71.8	1369	10 US-09-822-849A-67	Sequence 67, Appl
44	15.8	71.8	1787	10 US-09-925-302-3	Sequence 3, Appli
45	15.8	71.8	1923	10 US-09-822-849A-506	Sequence 506, App

ALIGNMENTS

RESULT 1
US-09-927-180-1
; Sequence 1, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO

us-09-270-437d-13.rnpb

Mon Apr 21 10:30:25 2003

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; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 96..2352
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-927-180-1
Query Match      88.2%; Score 19.4; DB 10; Length 2935;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCCTTTGGGACAGGAGGTC 22
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Db 2006 CTCCTTTGGGACAGGAGGTC 2026

RESULT 2
US-09-899-651-8
; Sequence 8, Application US/09899651
; Patent No. US20020111470A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 8
; LENGTH: 3283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-8

Query Match      88.2%; Score 19.4; DB 10; Length 3283;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21
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Db 132 GCTCTTTGGGACAGGAGGT 152

RESULT 3
US-09-899-651-6
; Sequence 6, Application US/09899651
; Patent No. US20020111470A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 8
; LENGTH: 3283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-8

Query Match      88.2%; Score 19.4; DB 10; Length 3283;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21
    |||||
Db 132 GCTCTTTGGGACAGGAGGT 152

RESULT 4
US-09-764-864-329
; Sequence 329, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 329
; LENGTH: 3694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-764-864-329

Query Match      88.2%; Score 19.4; DB 10; Length 3694;
Best Local Similarity 95.2%; Pred. No. 4.3;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21
    |||||
Db 132 GCTCTTTGGGACAGGAGGT 152

RESULT 5
US-10-071-223-1/c
; Sequence 1, Application US/10071223
; Patent No. US20020137174A1
; GENERAL INFORMATION:
; APPLICANT: Storm, Daniel R.
; APPLICANT: Hacker, Beth
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; APPLICANT: University of Washington
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYL
; FILE REFERENCE: 44481-5029-02-US
; CURRENT APPLICATION NUMBER: US/10/071,223
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 09/473,717
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/US98/13541
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/098,559
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,440
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4985
; TYPE: DNA
; FEATURE:
US-10-071-223-1/c
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; ORGANISM: human type IX adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)..(3898)
US-10-071-223-1

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Query Match	78.2%;	Score 17.2;	DB 12;	Length 4985;
Best Local Similarity	86.4%;	Pred. NO. 44;		
Matches 19; Conservative	0;	Mismatches 3;	Indels 0;	

QY 1 GCTCTTTGGGGACAGGAAGGTC 22
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Db 3751 GCACCTTTGGGTACAGGTAGGTC 3730

RESULT 6
US-09-751-100B-98/c
; Sequence 98, Application US/09751100B
; Patent No. US20020142436A1

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/ APPLICANT: Medical Research Council
/ TITLE OF INVENTION: Human Adenylylate Cyclase and Use Therefor
/ FILE REFERENCE: P27948A
/ CURRENT APPLICATION NUMBER: US/09/751.100B
/ CURRENT FILING DATE: 2000-12-28
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 98
/ LENGTH: 5515

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1 TYPE: DNA
2 ORGANISM: Homo sapiens
3 FEATURE:
4 NAME/KEY: CDS
5 LOCATION: (539)..(4600)
6 OTHER INFORMATION:
7 US-09-751-100B-98

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Query Match	78.2%	Score 17.2;	DB 10;	Length 5515;
Best Local Similarity	86.4%	Pred. No. 44;		
Matches 19; Conservative		0; Mismatches 3;	Indels 0;	

yy 1 GCTCTTTGGGACAGGAAGTC 22
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bb 4273 GCACCTTTGGGTACAGGTAGTC 4252

RESULT 7
 US-09-946-807-702/c
 Sequence 702, Application US/09946807
 Patent No. US20020165144A1
 GENERAL INFORMATION:
 APPLICANT: Stefansson, Hreinn
 APPLICANT: Steinhorsdottir, Valgerdur
 APPLICANT: Gulcher, Jeffrey R.
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
 FILE REFERENCE: 2345.2004-001
 CURRENT APPLICATION NUMBER: US/09/946, 807
 CURRENT FILING DATE: 2001-09-05
 PRIOR APPLICATION NUMBER: US/09/795,668
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: US/09/515,716
 PRIOR FILING DATE: 2000-02-28
 NUMBER OF SEQ ID NOS: 1531
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 702
 LENGTH: 401
 TYPE: DNA
 ORGANISM: Homo sapiens
 9-09-946-807-702

Query Match 76.4%; Score 16.8; DB 9; Length 401;
Best Local Similarity 90.0%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 2; Indels

Qy	3	TCTTTGGGGACAGGAAGTC	22
Db	98	TGTTTAGGGACAGGAAGTC	79

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RESULT 8
US/09-795-668-702/c
; Sequence 702, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn.
; APPLICANT: Steinhoradsdottir, valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795.668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 702
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-702

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Query Match	76.4%	Score 16.9;	DB 10;	Length 401;
Best Local Similarity	90.0%;	Pred. No. 75;		
Matches 18;	Conservative	0;	Mismatches 2;	Indels 0

QY	3	TCTTTGGGACAGGAAGGTC	22
Db	98	TGTTTAGGGACAGGAAGGTC	79

RESULT 9
US-09-795-686-702/c
Sequence 702, Application US/09795686
Patent No. US20020094954A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 702
LENGTH: 401
TYPE: DNA
ORGANISM: Homo sapiens
09-795-686-702

Query Match	76.4%	Score 16.8;	DB 10;	Length 401;
Best Local Similarity	90.0%	Pred. No. 75;		
Matches 18; Conservative	0;	Mismatches 2;	Indels 0	

3 TCATTGGGGACAGGAAGTC 22
98 TGTTTAGGGACAGGAAGTC 79

RESULT 10
S-09-858-546-3/c
Sequence 3, Application US/09858546
Patent NO. US20020172995A1
GENERAL INFORMATION:

us-09-270-437d-13.rnpb

Mon Apr 21 10:30:25 2003

APPLICANT: SHAO, Wei et al
 TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
 TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: CL001232
 CURRENT APPLICATION NUMBER: US/09/858,546
 CURRENT FILING DATE: 2001-05-17
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 80959
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(80959)
 OTHER INFORMATION: n = A,T,C or G
 US-09-858-546-3

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 Best Local Similarity 90.0%; Pred. No. 61;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGG 20
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 Db 75694 GCTCTTTGGGACAGGAGG 75675

RESULT 11
 US-10-125-540-600
 Sequence 600, Application US/10125540
 Publication No. US20030059875A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PT214CI
 CURRENT APPLICATION NUMBER: US/10/125,540
 CURRENT FILING DATE: 2002-04-19
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 646
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 600
 LENGTH: 15531
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-125-540-600

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 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 12698 TCTTTGGGACAGGAGG 12715

RESULT 12
 US-09-764-870-600
 Sequence 600, Application US/09764870
 Patent No. US20020042386A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PT214
 CURRENT APPLICATION NUMBER: US/09/764,870
 CURRENT FILING DATE: 2001-01-17
 Prior application data removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 646
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 600
 LENGTH: 15531
 TYPE: DNA
 ORGANISM: Homo sapiens

US-09-764-870-600

Query Match 74.5%; Score 16.4; DB 10; Length 15531;
 Best Local Similarity 94.4%; Pred. No. 99;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCTTTGGGACAGGAGG 20
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 Db 12698 TCTTTGGGACAGGAGG 12715

RESULT 13
 US-09-771-208-20
 Sequence 20, Application US/09771208
 Patent No. US20020155564A1.
 GENERAL INFORMATION:
 APPLICANT: MEDRANO, JUAN
 APPLICANT: BRADFORD, ERIC
 APPLICANT: HORVAT, SIMON
 TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
 FILE REFERENCE: 407T-923710US
 CURRENT APPLICATION NUMBER: US/09/771,208
 CURRENT FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: US 08/999,477
 PRIOR FILING DATE: 1997-12-29
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 20
 LENGTH: 659158
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (123459)..(123478)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 LOCATION: (602466)..(602485)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 LOCATION: (546998)..(547017)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 LOCATION: (494715)..(494814)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 LOCATION: (390986)..(391005)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 LOCATION: (346860)..(346823)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 LOCATION: (317174)..(317193)
 OTHER INFORMATION: n is unidentified a, c, g, or t
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 OTHER INFORMATION: n is unidentified a, c, g, or t
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 LOCATION: (271829)..(271848)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 LOCATION: (183872)..(183891)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 LOCATION: (170625)..(170645)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 LOCATION: (132680)..(132700)
 OTHER INFORMATION: n is unidentified a, c, g, or t
 NAME/KEY: misc_feature
 OTHER INFORMATION: n is a, c, g, or t
 US-09-771-208-20

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Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Job time : 206.5 secs

QY 4 CTTTGGGACAGGAAGGT 21
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Db 39002 CTTTGGGACAGGAAGGT 39019

RESULT 14
US-09-878-574-5931
; Sequence 5931, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 5931
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701097533H1
US-09-878-574-5931

Query Match 73.6%; Score 16.2; DB 10; Length 256;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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|||||
Db 145 GCGCCTTGGGACAGGAAGGT 165

RESULT 15
US-09-878-574-9673
; Sequence 9673, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 9673
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701102760H1
US-09-878-574-9673

Query Match 73.6%; Score 16.2; DB 10; Length 275;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAAGGT 21
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Db 120 GCGCCTTGGGACAGGAAGGT 140

Search completed: April 18, 2003, 10:16:02

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 05:48:17 ; Search time 1211 Seconds
(without alignments)
456.759 Million cell updates/sec

Title: US-09-270-437D-13

Perfect score: 22

Sequence: 1 gctcttggggacaggaagtc 22

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Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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- 85: /cgn2_6/ptodata/1/pna/US6041 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	19.4	88.2	270	13	US-08-993-774-322
5	19.4	88.2	270	20	US-09-539-800-7233
6	19.4	88.2	270	20	US-09-539-800B-7233
7	19.4	88.2	270	20	US-09-539-800C-7233
8	19.4	88.2	270	47	US-60-034-975-322
9	19.4	88.2	321	25	US-09-540-208-54639
10	19.4	88.2	345	21	US-09-540-208-54639
11	19.4	88.2	384	17	US-09-399-932-3999
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13	19.4	88.2	408	39	US-10-092-302-369
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16	19.4	88.2	417	35	US-09-933-524A-48934
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18	19.4	88.2	458	5	US-08-196-362A-7619
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					Sequence 1160, App
					Sequence 29243, A
					Sequence 322, App
					Sequence 7233, App
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Mon Apr 21 10:30:26 2003

us-09-270-437d-13.rnnp

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23 19.4 88.2 465 17 US-09-304-649-680
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27 19.4 88.2 467 35 US-09-933-524A-49810
28 19.4 88.2 546 56 US-60-125-787-430
29 19.4 88.2 598 62 PCT-US01-08631-6785
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ALIGNMENTS

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RESULT 1
US-09-540-229-481
; Sequence 481, Application US/09540229
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
; FILE REFERENCE: PD-1033 CIP
; CURRENT APPLICATION NUMBER: US/09/540,229
; CURRENT FILING DATE: 2000-03-31
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 193582
; SOFTWARE: PERL Program
; SEQ ID NO 481
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00195332
; NAME/KEY: unsure
; LOCATION: 2, 11, 23-24, 33, 35, 39, 54, 94-95, 101, 113-114, 173, 182, 194, 198,
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-229-481

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Query Match 88.2%; Score 19.4; DB 21; Length 231;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GCTCTTTGGGACAGGAAGT 21
Db 119 GCTCTTTGGGACAGGAAGT 139

RESULT 2
US-08-903-802-1160
; Sequence 1160, Application US/08903802
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.

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; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerbloom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
; TITLE OF INVENTION: DERIVED FROM HUMAN BLADDER
; NUMBER OF SEQUENCES: 1441
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION NUMBER: US/08/903,802
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/023,308
; FILING DATE: JULY 31, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0202 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 1160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONE: 1322001
US-08-903-802-1160

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Query Match 88.2%; Score 19.4; DB 13; Length 237;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GCTCTTTGGGACAGGAAGT 21
Db 143 GCTCTTTGGGACAGGAAGT 163

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RESULT 3
US-09-540-210B-29243
; Sequence 29243, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP
; CURRENT APPLICATION NUMBER: US/09/540,210B
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/972,899
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/395,244

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; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/722,922
; PRIOR FILING DATE: September 27, 1996
; PRIOR APPLICATION NUMBER: 60/005,526
; PRIOR FILING DATE: September 29, 1995
; PRIOR APPLICATION NUMBER: 08/824,029
; PRIOR FILING DATE: March 25, 1997
; PRIOR APPLICATION NUMBER: 60/014,010
; PRIOR FILING DATE: March 25, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/903,555
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/862,178
; PRIOR FILING DATE: May 22, 1997
; PRIOR APPLICATION NUMBER: 60/018,217
; PRIOR FILING DATE: May 23, 1996
; PRIOR APPLICATION NUMBER: 08/881,589
; PRIOR FILING DATE: June 24, 1997
; PRIOR APPLICATION NUMBER: 60/021,275
; PRIOR FILING DATE: June 25, 1996
; PRIOR APPLICATION NUMBER: 08/903,802
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/905,881
; PRIOR FILING DATE: August 1, 1997
; PRIOR APPLICATION NUMBER: 60/025,204
; PRIOR FILING DATE: August 1, 1996
; PRIOR APPLICATION NUMBER: 08/903,471
; PRIOR FILING DATE: July 30, 1997
; PRIOR APPLICATION NUMBER: 60/025,478
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/903,556
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/025,217
; PRIOR FILING DATE: August 22, 1996
; PRIOR APPLICATION NUMBER: 08/937,142
; PRIOR FILING DATE: September 23, 1997
; PRIOR APPLICATION NUMBER: 60/026,598
; PRIOR FILING DATE: September 24, 1996
; PRIOR APPLICATION NUMBER: 08/960,746
; PRIOR FILING DATE: October 29, 1997
; PRIOR APPLICATION NUMBER: 60/030,144
; PRIOR FILING DATE: October 30, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/755,524
; PRIOR FILING DATE: November 22, 1996
; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997

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; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 29243
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00029997
US-09-540-210B-29243

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Query Match      88.2%; Score 19.4; DB 21; Length 237;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GCTCTTTGGGACAGGAGGT 21
    |||||
Db 143 GCTCTTTGGGACAGGAGCT 163

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RESULT 4
US-08-993-774-322
; Sequence 322, Application US/08993774
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerbloom, Ingrid B.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MESENTERY TUMOR
; NUMBER OF SEQUENCES: 4086
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,774
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0300P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 322:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs

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Mon Apr 21 10:30:26 2003

us-09-270-437d-13.rnmpm

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 2502822H1
US-08-993-774-322

Query Match 88.2%; Score 19.4; DB 13; Length 270;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCTCTTTGGGACAGGAAGCT 21
Db 111 GCTCTTTGGGACAGGAAGCT 131

RESULT 5
US-09-539-800-7233
; Sequence 7233, Application US/09539800
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
; FILE REFERENCE: PD-1023 CIP
; CURRENT APPLICATION NUMBER: US/09/539,800
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: August 16, 1995
; PRIOR FILING DATE: August 16, 1995
; PRIOR FILING DATE: June 27, 1994
; PRIOR FILING DATE: November 4, 1994
; PRIOR FILING DATE: November 4, 1994
; PRIOR FILING DATE: October 3, 1997
; PRIOR FILING DATE: October 3, 1997
; PRIOR FILING DATE: October 3, 1997
; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: October 4, 1997
; PRIOR FILING DATE: October 4, 1997
; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: December 18, 1997
; PRIOR FILING DATE: December 18, 1997
; PRIOR FILING DATE: December 20, 1996
; PRIOR FILING DATE: December 20, 1996
; PRIOR FILING DATE: February 10, 1999
; PRIOR FILING DATE: February 10, 1999
; PRIOR FILING DATE: February 12, 1998
; PRIOR FILING DATE: February 12, 1998
; PRIOR FILING DATE: February 12, 1998
; PRIOR FILING DATE: December 1, 1999
; PRIOR FILING DATE: December 1, 1999
; PRIOR FILING DATE: December 10, 1998
; PRIOR FILING DATE: December 10, 1998
; NUMBER OF SEQ ID NOS: 19698
; SOFTWARE: PERL Program
; SEQ ID NO 7233
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00328727

US-09-539-800-7233
; Sequence 7233, Application US/09539800
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
; FILE REFERENCE: PD-1023 CIP
; CURRENT APPLICATION NUMBER: US/09/539,800
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: August 16, 1995
; PRIOR FILING DATE: August 16, 1995
; PRIOR FILING DATE: June 27, 1994
; PRIOR FILING DATE: November 4, 1994
; PRIOR FILING DATE: November 4, 1994
; PRIOR FILING DATE: October 3, 1997
; PRIOR FILING DATE: October 3, 1997
; PRIOR FILING DATE: October 3, 1997
; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: October 4, 1997
; PRIOR FILING DATE: October 4, 1997
; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: December 18, 1997
; PRIOR FILING DATE: December 18, 1997
; PRIOR FILING DATE: December 20, 1996
; PRIOR FILING DATE: December 20, 1996
; PRIOR FILING DATE: February 10, 1999
; PRIOR FILING DATE: February 10, 1999
; PRIOR FILING DATE: February 12, 1998
; PRIOR FILING DATE: February 12, 1998
; PRIOR FILING DATE: February 12, 1998
; PRIOR FILING DATE: December 1, 1999
; PRIOR FILING DATE: December 1, 1999
; PRIOR FILING DATE: December 10, 1998
; PRIOR FILING DATE: December 10, 1998
; NUMBER OF SEQ ID NOS: 19698
; SOFTWARE: PERL Program
; SEQ ID NO 7233
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00328727

Query Match 88.2%; Score 19.4; DB 20; Length 270;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCTCTTTGGGACAGGAAGCT 21

Db 111 GCTCTTTGGGACAGGAAGCT 131

RESULT 6
US-09-539-800B-7233
; Sequence 7233, Application US/09539800B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
; FILE REFERENCE: PD-1023 CIP
; CURRENT APPLICATION NUMBER: US/09/539,800B
; PRIOR FILING DATE: 2000-03-30
; PRIOR FILING DATE: August 16, 1995
; PRIOR FILING DATE: August 16, 1995
; PRIOR FILING DATE: June 27, 1994
; PRIOR FILING DATE: November 4, 1994
; PRIOR FILING DATE: November 4, 1994
; PRIOR FILING DATE: October 3, 1997
; PRIOR FILING DATE: October 3, 1997
; PRIOR FILING DATE: October 3, 1997
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; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: October 4, 1996
; PRIOR FILING DATE: December 18, 1997
; PRIOR FILING DATE: December 18, 1997
; PRIOR FILING DATE: December 20, 1996
; PRIOR FILING DATE: December 20, 1996
; PRIOR FILING DATE: February 10, 1999
; PRIOR FILING DATE: February 10, 1999
; PRIOR FILING DATE: February 12, 1998
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; PRIOR FILING DATE: December 1, 1999
; PRIOR FILING DATE: December 1, 1999
; PRIOR FILING DATE: December 10, 1998
; PRIOR FILING DATE: December 10, 1998
; NUMBER OF SEQ ID NOS: 19698
; SOFTWARE: PERL Program
; SEQ ID NO 7233
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00328727

US-09-539-800B-7233

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US-09-539-800B-7233

US-09-539-800B-7233

US-09-539-800B-7233

US-09-539-800B-7233

APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800C
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/521,383
PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
PRIOR FILING DATE: November 4, 1994
PRIOR APPLICATION NUMBER: 08/943,978
PRIOR FILING DATE: October 3, 1997
PRIOR APPLICATION NUMBER: 60/028,732
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/943,979
PRIOR FILING DATE: October 4, 1997
PRIOR APPLICATION NUMBER: 60/027,782
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/993,774
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/034,975
PRIOR FILING DATE: December 20, 1996
PRIOR APPLICATION NUMBER: 09/250,003
PRIOR FILING DATE: February 10, 1999
PRIOR APPLICATION NUMBER: 60/074,364
PRIOR FILING DATE: February 12, 1998
PRIOR APPLICATION NUMBER: 09/452,747
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: 60/111,910
PRIOR FILING DATE: December 10, 1998
SOFTWARE: PERL Program
SEQ ID NO 7233
LENGTH: 270
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: hu00328727
US-09-539-800C-7233

Query Match 88.2%; Score 19.4; DB 20; Length 270;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21
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DB 111 GCTCTTTGGGACAGGAGGT 131

RESULT 8
US-60-034-975-322
Sequence 322, Application US/60034975
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: MESENTERY TUMOR
NUMBER OF SEQUENCES: 4086
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/034,975
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0300P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 322:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 2502822H1
US-60-034-975-322

Query Match 88.2%; Score 19.4; DB 47; Length 270;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21
|||||
DB 111 GCTCTTTGGGACAGGAGGT 131

RESULT 9
US-09-644-871-2566
Sequence 2566, Application US/09644871
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1167-001
CURRENT APPLICATION NUMBER: US/09/644,871
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,059
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9739
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2566
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(321)
OTHER INFORMATION: n = A,T,C or G
US-09-644-871-2566

Query Match 88.2%; Score 19.4; DB 25; Length 321;
Best Local Similarity 95.2%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21
|||||
DB 122 GCTCTTTGGGACAGGAGGT 142

RESULT 10
US-09-540-208-54639
Sequence 54639, Application US/09540208

Mon Apr 21 10:30:26 2003

us-09-270-437d-13.rnnp

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GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleageane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF MALE REPRODUCTIVE TISSUE
FILE REFERENCE: PD-1029 CIP
CURRENT APPLICATION NUMBER: US/09/540,208
CURRENT FILING DATE: 2000-03-31
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 70811
SOFTWARE: PERL Program
SEQ ID NO 54639
LENGTH: 345
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc feature
NAME/KEY: misc feature
OTHER INFORMATION: incyte ID No: hu01153334
US-09-540-208-54639

Query Match      88.2%; Score 19.4; DB 21; Length 345;
Best Local Similarity 95.2%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAGGT 21
    |||||
Db 151 GCTCTTTGGGACAGGAGCT 171

PCT-US01-01307-369
; Sequence 369, Application PC/TUS0101307
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT218PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01307
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 369
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (337)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (363)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (385)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
; PCT-US01-01307-369

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Query Match      88.2%; Score 19.4; DB 1; Length 408;
Best Local Similarity 95.2%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 GCTCTTTGGGACAGGAGGT 21
    |||||
Db 65 GCTCTTTGGGACAGGAGCT 85

RESULT 13
US-10-092-302-369
; Sequence 369, Application US/10092302
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT218C1
; CURRENT APPLICATION NUMBER: US/10/092,302
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 1040
; Prior application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 369
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (124)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (328)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (337)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (363)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (385)

```

```

GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleageane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF MALE REPRODUCTIVE TISSUE
FILE REFERENCE: PD-1029 CIP
CURRENT APPLICATION NUMBER: US/09/540,208
CURRENT FILING DATE: 2000-03-31
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 70811
SOFTWARE: PERL Program
SEQ ID NO 54639
LENGTH: 345
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc feature
NAME/KEY: misc feature
OTHER INFORMATION: incyte ID No: hu01153334
US-09-540-208-54639

Query Match      88.2%; Score 19.4; DB 21; Length 345;
Best Local Similarity 95.2%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAGGT 21
    |||||
Db 151 GCTCTTTGGGACAGGAGCT 171

```

```

RESULT 11
US-09-399-932-3999
; Sequence 3999, Application US/09399932
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN BURKITT'S LYMPHOMA LIBRARY
; FILE REFERENCE: MLN98-47PM
; CURRENT APPLICATION NUMBER: US/09/399,932
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100,464
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/101,670
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106,456
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/126,902
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/132,067
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/144,447
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 5743
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3999
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-399-932-3999

```

```

Query Match      88.2%; Score 19.4; DB 17; Length 384;
Best Local Similarity 95.2%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAGGT 21
    |||||
Db 130 GCTCTTTGGGACAGGAGCT 150

RESULT 12

```

```
; OTHER INFORMATION: n equals a,t,g, or c
US-10-092-302-369

Query Match      88.2%; Score 19.4; DB 39; Length 408;
Best Local Similarity 95.2%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAAGCT 21
    |||||
Db 65 GCTCTTTGGGACAGGAAGCT 85
    |||||

RESULT 14
US-09-528-409-48934
; Sequence 48934, Application US/09528409
; GENERAL INFORMATION:
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark
; APPLICANT: Jones, Lee W.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 774
; CURRENT APPLICATION NUMBER: US/09/528,409
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,453
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 116231
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 48934
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(417)
; OTHER INFORMATION: n = A,T,C or G
US-09-528-409-48934

Query Match      88.2%; Score 19.4; DB 19; Length 417;
Best Local Similarity 95.2%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAAGCT 21
    |||||
Db 117 GCTCTTTGGGACAGGAAGCT 137
    |||||

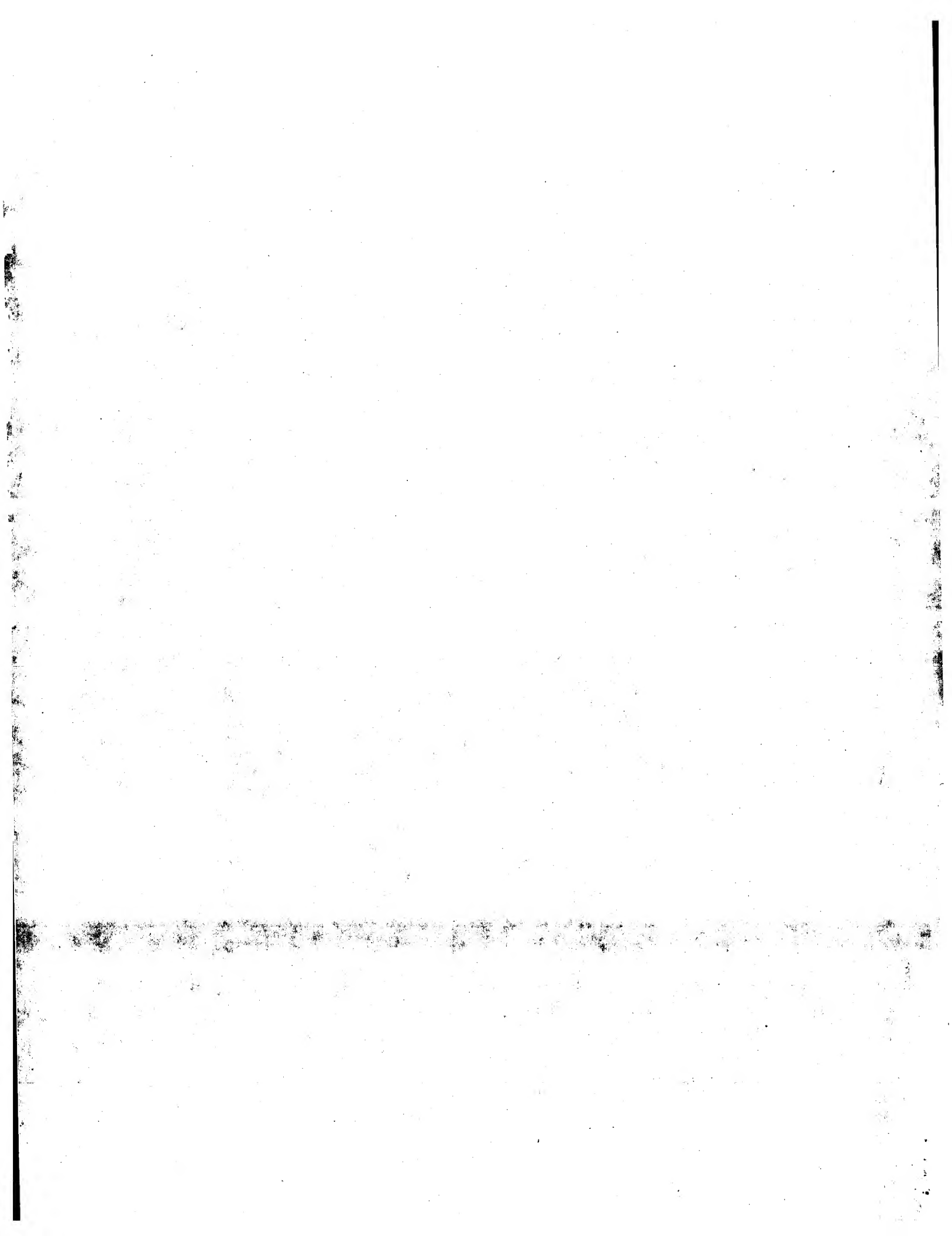
RESULT 15
US-09-933-524-48934
; Sequence 48934, Application US/09933524
; GENERAL INFORMATION:
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark
; APPLICANT: Jones, Lee W.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 774
; CURRENT APPLICATION NUMBER: US/09/933,524
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 09/528,409
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 116231
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 48934
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)...(417)
; OTHER INFORMATION: n = A,T,C or G
US-09-933-524-48934

Query Match      88.2%; Score 19.4; DB 35; Length 417;
Best Local Similarity 95.2%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAAGCT 21
    |||||
Db 117 GCTCTTTGGGACAGGAAGCT 137
    |||||
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Search completed: April 18, 2003, 09:35:47
Job time : 1212 secs



GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:28 ; Search time 245.167 Seconds
(without alignment)
400.770 Million cell updates/sec

Title: US-09-270-437D-13

Perfect score: 22
Sequence: 1 gctctttgggacaggaagtc 22

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5897297 seqs, 2233080881 residues

Total number of hits satisfying chosen parameters: 11794594

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	5	US-09-270-437D-13
2	19.4	88.2	364	6	US-09-513-999C-3265
3	19.4	88.2	458	6	US-09-912-293-228701
4	19.4	88.2	871	6	US-09-724-676-8826
5	19.4	88.2	871	6	US-09-724-676A-8826
6	19.4	88.2	1707	1	PCT-US02-31357-39
7	19.4	88.2	1707	9	US-10-262-445-39
8	19.4	88.2	3237	8	US-10-170-235-5179
9	19.4	88.2	3237	11	US-60-452-680-612
10	19.4	88.2	3237	11	US-60-453-135-482
11	19.4	88.2	3237	11	US-60-453-050-482
12	19.4	88.2	3283	5	US-09-270-437D-8
13	19.4	88.2	3412	5	US-09-270-437D-6
14	19.4	88.2	3427	8	US-10-170-235-21870
15	19.4	88.2	3427	11	US-60-453-135-3834
16	19.4	88.2	3427	11	US-60-453-050-3834
17	19.4	88.2	3445	11	US-60-452-680-3237
18	19.4	88.2	3475	8	US-10-170-235-22086
19	19.4	88.2	3475	11	US-60-453-135-3835
20	19.4	88.2	3475	11	US-60-453-050-3835
21	18.8	85.5	30922	7	US-09-949-016-16700
22	18.4	83.6	598359	7	US-09-947-911-215

23	18	81.8	84839	7	US-09-949-016-15816	Sequence 15816, A
24	17.8	80.9	9968	7	US-09-949-016-12472	Sequence 12472, A
25	17.8	80.9	9969	7	US-09-949-016-15903	Sequence 15903, A
26	17.4	79.1	403	6	US-09-912-293-3245	Sequence 96328, A
27	17.4	79.1	474	6	US-09-912-293-3245	Sequence 3245, Ap
28	17.4	79.1	4101	9	US-10-144-771-20672	Sequence 20672, A
29	17.2	78.2	201	10	US-60-455-444-42575	Sequence 42575, A
30	17.2	78.2	201	11	US-60-453-135-70940	Sequence 70940, A
31	17.2	78.2	201	11	US-60-453-050-70940	Sequence 70940, A
32	17.2	78.2	442	6	US-09-534-850-18297	Sequence 18297, A
33	17.2	78.2	2580	9	US-10-092-900A-153	Sequence 153, App
34	17.2	78.2	2890	8	US-10-170-235-32027	Sequence 32027, A
35	17.2	78.2	2890	11	US-60-441-839-137	Sequence 137, App
36	17.2	78.2	2890	11	US-60-452-680-9301	Sequence 9301, Ap
37	17.2	78.2	2890	11	US-60-453-135-5460	Sequence 5460, Ap
38	17.2	78.2	2890	11	US-60-453-050-5460	Sequence 5460, Ap
39	17.2	78.2	3560	9	US-10-338-044-2260	Sequence 2260, Ap
40	17.2	78.2	4933	1	PCT-US03-05336-52	Sequence 52, Appl
41	17.2	78.2	4946	8	US-10-170-235-40560	Sequence 40560, A
42	17.2	78.2	4985	7	US-09-949-016-152	Sequence 152, App
43	17.2	78.2	6532	8	US-10-170-235-23701	Sequence 23701, A
44	17.2	78.2	6532	10	US-60-455-444-3409	Sequence 3409, Ap
45	17.2	78.2	6532	11	US-60-453-135-6603	Sequence 6603, Ap

ALIGNMENTS

RESULT 1
US-09-270-437D-13
; Sequence 13, Application US/09270437D
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen
; FILE REFERENCE: LUD 5538.1
; CURRENT APPLICATION NUMBER: US/09/270,437D
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/061,709
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-270-437D-13

Query Match 100.0%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAGGTC 22
Db 1 GCTCTTTGGGACAGGAGGTC 22

RESULT 2
US-09-513-999C-3265
; Sequence 3265, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C

Mon Apr 21 10:30:28 2003

us-09-270-437d-13.rnnpn

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; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3265
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..363
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 17
; OTHER INFORMATION: k=g or t
; US-09-513-999C-3265
;
; Query Match      88.2%; Score 19.4; DB 6; Length 364;
; Best Local Similarity 95.2%; Pred. No. 30;
; Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 GCTCTTTGGGGACAGGAAGGT 21
; DB 135 GCTCTTTGGGGACAGGAAGCT 155
;
; RESULT 3
; US-09-912-293-228701
; Sequence 228701, Application US/09912293
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
; FILE REFERENCE: PO-100
; CURRENT APPLICATION NUMBER: US/09/912,293
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 08/103,744
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 09/249,651
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 08/104,507
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 08/196,363
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 09/859,490
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 08/196,362
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 08/221,623
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 08/220,691
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 09/741,830
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/813,155
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 244538
; SEQ ID NO 228701
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (52)..(52)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (58)..(58)
; OTHER INFORMATION: n is equal to a,t,g, or c
;
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (87)..(87)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109)..(110)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (204)..(204)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (213)..(214)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (222)..(222)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (226)..(226)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (263)..(263)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (323)..(323)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (335)..(335)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (349)..(349)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (352)..(353)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (356)..(357)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (360)..(360)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (363)..(363)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (369)..(369)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (380)..(380)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (384)..(384)
; OTHER INFORMATION: n is equal to a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (387)..(387)
; OTHER INFORMATION: n is equal to a,t,g, or c

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FEATURE:
NAME/KEY: misc feature
LOCATION: (403)..(403)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (410)..(410)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (416)..(416)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (419)..(419)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (428)..(428)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (435)..(435)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (457)..(457)
OTHER INFORMATION: n is equal to a,t,g, or c
US-09-912-293-228701
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```
Query Match      88.2%; Score 19.4; DB 6; Length 458;
Best Local Similarity 95.2%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 GCTCTTTGGGGACAGGAAGGT 21
    |||||||
Db 150 GCTCTTTGGGGACAGGAAGCT 170
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RESULT 4

```
US-09-724-676-8826/c
Sequence 8826, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8826
LENGTH: 871
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-8826
```

```
Query Match      88.2%; Score 19.4; DB 6; Length 871;
Best Local Similarity 95.2%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 GCTCTTTGGGGACAGGAAGGT 21
    |||||||
Db 374 GCTCTTTGGGGACAGGAAGCT 354
```

RESULT 5

```
US-09-724-676A-8826/c
Sequence 8826, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
```

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FEATURE:
NAME/KEY: misc feature
LOCATION: (403)..(403)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (410)..(410)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (416)..(416)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (419)..(419)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (428)..(428)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (435)..(435)
OTHER INFORMATION: n is equal to a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (457)..(457)
OTHER INFORMATION: n is equal to a,t,g, or c
US-09-724-676A-8826
```

```
Query Match      88.2%; Score 19.4; DB 6; Length 871;
Best Local Similarity 95.2%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 GCTCTTTGGGGACAGGAAGGT 21
    |||||||
Db 374 GCTCTTTGGGGACAGGAAGCT 354
```

RESULT 6

```
PCT-US02-31357-39
Sequence 39, Application PC/TUS0231357
GENERAL INFORMATION:
APPLICANT: Curagen Corporation, et al
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
FILE REFERENCE: 21402-462D-061
CURRENT APPLICATION NUMBER: PCT/US02/31357
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/327,454
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,849
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/329,414
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/330,142
PRIOR FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/341,058
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/343,629
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/349,575
PRIOR FILING DATE: 2001-10-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 39
LENGTH: 1707
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (5)..(1669)
PCT-US02-31357-39
```

```
Query Match      88.2%; Score 19.4; DB 1; Length 1707;
Best Local Similarity 95.2%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 GCTCTTTGGGGACAGGAAGGT 21
    |||||||
Db 67 GCTCTTTGGGGACAGGAAGCT 87
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RESULT 7

```
US-10-262-445-39
Sequence 39, Application US/10262445
GENERAL INFORMATION:
```

QY 1 GCCTCTTTGGGGACAGGAAGT 21

Db 76 GCTCTTTGGGACAGGAAGCT 96

RESULT 11

US-60-453-050-482
; Sequence 482, Application US/60453050
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: LUKE, May

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/60/453,050

; CURRENT FILING DATE: 2003-03-10

; NUMBER OF SEQ ID NOS: 82762

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 482

; LENGTH: 3237

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-453-050-482

Query Match 88.2%; Score 19.4; DB 11; Length 3237;

Best Local Similarity 95.2%; Pred. No. 38;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAAGCT 21

Db 76 GCTCTTTGGGACAGGAAGCT 96

RESULT 12

US-09-270-437D-8

; Sequence 8, Application US/09270437D

; GENERAL INFORMATION:

; APPLICANT: Chen, Yao-Tseng

; APPLICANT: Gure, Ali

; APPLICANT: Tsang, Solam

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Jager, Elke

; APPLICANT: Knuth, Alexander

; APPLICANT: Old, Lloyd J.

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antige

; FILE REFERENCE: Antigenes Per Se, And Uses Thereof

; CURRENT APPLICATION NUMBER: US/09/270,437D

; CURRENT FILING DATE: 1999-03-16

; PRIOR FILING DATE: 09/061,709

; NUMBER OF SEQ ID NOS: 23

; SEQ ID NO 8

; LENGTH: 3283

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 3243

; OTHER INFORMATION: unsure of nucleotide

US-09-270-437D-8

Query Match

Best Local Similarity 88.2%; Score 19.4; DB 5; Length 3283;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAAGCT 21

Db 132 GCTCTTTGGGACAGGAAGCT 152

RESULT 13

US-09-270-437D-6

; Sequence 6, Application US/09270437D

; GENERAL INFORMATION:

; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antiger
; FILE REFERENCE: Antigenes Per Se, And Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/270,437D
; CURRENT FILING DATE: 1999-03-16
; PRIOR FILING DATE: 09/061,709
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 6
; LENGTH: 3412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3372
; OTHER INFORMATION: unsure of nucleotide
US-09-270-437D-6

Query Match 88.2%; Score 19.4; DB 5; Length 3412;

Best Local Similarity 95.2%; Pred. No. 39;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAAGCT 21

Db 132 GCTCTTTGGGACAGGAAGCT 152

RESULT 14

US-10-170-235-21870

; Sequence 21870, Application US/10170235

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig

; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN

; FILE REFERENCE: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF

; CURRENT APPLICATION NUMBER: US/10/170,235

; CURRENT FILING DATE: 2003-03-17

; NUMBER OF SEQ ID NOS: 42514

; SEQ ID NO 21870

; LENGTH: 3427

; TYPE: DNA

; ORGANISM: HUMAN

US-10-170-235-21870

Query Match

Best Local Similarity 88.2%; Score 19.4; DB 8; Length 3427;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAAGCT 21

Db 130 GCTCTTTGGGACAGGAAGCT 150

RESULT 15

US-60-453-135-3834

; Sequence 3834, Application US/60453135

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: IAKOUBOVA, Olga

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/60/453,135

; CURRENT FILING DATE: 2003-03-10

; NUMBER OF SEQ ID NOS: 82762

; SOFTWARE: FastSeq for Windows Version 4.0

us-09-270-437d-13.rnpn

Mon Apr 21 10:30:28 2003

```

; SEQ ID NO 3834
; LENGTH: 3427
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-3834

Query Match      88.2%; Score 19.4; DB 11; Length 3427;
Best Local Similarity 95.2%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY . 1 GCTCTTTGGGGACAGGAAGCT 21
    |||||
Db 130 GCTCTTTGGGGACAGGAAGCT 150

```

Search completed: April 18, 2003, 10:50:31
Job time : 249.167 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:47:40 ; Search time 766 Seconds
(without alignments)
465.145 Million cell updates/sec

Title: US-09-270-437d-13

Perfect score: 22
Sequence: 1 gctcttggggacaggaaggtc 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estini:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	88.2	330	9	AA226813
2	19.4	88.2	453	9	AL121466
3	19.4	88.2	478	12	BG007027
4	19.4	88.2	479	14	H66979
5	19.4	88.2	620	12	BF914566
6	19.4	88.2	851	14	BQ221568

7	19.4	88.2	874	12	BG481336
8	19.4	88.2	889	12	BG748346
9	18.8	85.5	264	13	BI971125
10	18.8	85.5	309	13	BM484358
11	18.8	85.5	373	12	BF189397
12	18.8	85.5	471	9	AI623653
13	18.4	83.6	566	17	BH261805
14	18.4	83.6	680	17	BH098064
15	18.4	83.6	856	12	BG480515
16	18.4	83.6	2768	11	BC015720
17	18	81.8	738	17	P0222C03U
18	18	81.8	861	17	BQ706255
19	18	81.8	1742	11	AK015621
20	17.8	80.9	299	9	AL597676
21	17.8	80.9	368	10	B8872349
22	17.8	80.9	429	14	Z84036
23	17.8	80.9	434	10	B8863724
24	17.8	80.9	448	10	B8852457
25	17.8	80.9	449	13	BM253624
26	17.8	80.9	458	10	B8852318
27	17.8	80.9	469	10	B8853640
28	17.8	80.9	489	10	B8855310
29	17.8	80.9	528	13	BM107521
30	17.8	80.9	541	14	BQ770242
31	17.8	80.9	582	14	BQ235601
32	17.8	80.9	617	10	B8660288
33	17.8	80.9	649	17	AZ650694
34	17.8	80.9	668	10	B8618315
35	17.8	80.9	673	12	BG768944
36	17.8	80.9	715	17	AG142970
37	17.8	80.9	815	13	BI688088
38	17.8	80.9	1146	13	BM484345
39	17.4	79.1	140	10	BE221716
40	17.4	79.1	150	10	BB163693
41	17.4	79.1	150	10	BB191260
42	17.4	79.1	152	10	BB363001
43	17.4	79.1	154	10	BB438580
44	17.4	79.1	154	10	B8527579
45	17.4	79.1	155	10	B8515762

ALIGNMENTS

RESULT 1
AA226813
LOCUS
DEFINITION
zr18f09.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens
CDNA clone IMAGE:663785 5', mRNA sequence.
ACCESSION
AA226813
VERSION
AA226813.1 GI:1848349
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 330)
AUTHORS
Hillier L., Lennon G., Becker M., Bonaldo M.P., Chiapelli B., Chissoe S., Dietrich N., Dubuque T., Favello A., Gish W., Hawkins M., Hultman M., Kucaba T., Lacy M., Le M., Le N., Mardis E., Moore B., Morris M., Parsons J., Prange C., Rifkin L., Rohlfing T., Schellenberg K., Soares M.B., Tan F., Thierry-Mieg J., Trevaskis E., Underwood K., Wohlmann P., Waterston R., Wilson R. and Marra M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the

Mon Apr 21 10:30:29 2003

IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 321.

FEATURES

source

1. 330
/organism="Homo sapiens"
/db_xref="GDB:5589715"
/db_xref="taxon:9606"
/clone="IMAGE:663785"
/clone_lib="Stratagene NT2 neuronal precursor 937230"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: brain; Vector: pBluescript SK-; Site: 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
oligo dt. Uninduced, exponentially growing neuroepithelial
cells (Ntera-2/ci.D1). Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

BASE COUNT
ORIGIN

Query Match 88.2%; Score 19.4; DB 9; Length 330;
Best Local Similarity 95.2%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21

|||||

DB 109 GCTCTTTGGGACAGGAGGT 129

RESULT 2

AL121466

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

453 bp mRNA linear EST 25-FEB-2000
DKFZp762L097_r1 762 (synonym: hmcl2) Homo sapiens cDNA clone
AL121466
DKFZp762L097 5', mRNA sequence.

AL121466.1 GI:5927467
EST.
human.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 453)
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

EST (Ottewaelder, et al.)
Unpublished (1999)
Contact: Ottewaelder B
MIPS

Am Klopferpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medicenmix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No 81 sequence

available.
This clone (DKFZp762L097) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1. 453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762L097"
/clone_lib="hmcl2" (synonym: hmcl2)
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT

ORIGIN

117 a 121 c 137 g 78 t

Query Match 88.2%; Score 19.4; DB 9; Length 453;

Best Local Similarity 95.2%; Pred. No. 1.8e+02;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21

|||||

DB 118 GCTCTTTGGGACAGGAGGT 138

RESULT 3

BG007027/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BG007027 478 bp mRNA linear EST 24-JAN-2001
RC1-GN0235-271100-021-a10 GN0235 Homo sapiens cDNA, mRNA sequence.

BG007027
BG007027.1 GI:12450789
EST.
human.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 478)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Sucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-GN0235-
271100-021-a10&t3=2000-11-27&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 45
High quality sequence stop: 478.

Location/Qualifiers
1. 478
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0235"
/dev_stage="Adult"

/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI
; Site 2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT 135 a 127 c 87 g 129 t

ORIGIN

Query Match 88.2%; Score 19.4; DB 12; Length 478;
Best Local Similarity 95.2%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCTTTGGGACAGGAGGT 21

|||||

DB 474 GCTCTTTGGGACAGGAGGT 454

RESULT 4

H66979

LOCUS H66979 479 bp mRNA linear EST 18-OCT-1995
DEFINITION yu17a11.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone
IMAGE:234044 5' similar to contains Alu repetitive element; , mRNA
sequence.
ACCESSION H66979.1 GI:1025719
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,
R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
COMMENT Contact: wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1511
High quality sequence stops: 401
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1511 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 401.
Location/Qualifiers
1. .479
/organism="Homo sapiens"
/db_xref="GDB:378721"
/db_xref="taxon:9606"
/clone="IMAGE:234044"
/clone_lib="Soares fetal liver spleen INFILS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: p7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACTGAGATATATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 111 a 100 c 117 g 142 t 9 others
ORIGIN

Query Match 88.2%; Score 19.4; DB 14; Length 479;
Best Local Similarity 95.2%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTCTTTGGGACAGGAGCT 21
|||||
Db 103 GCTCTTTGGGACAGGAGCT 123

RESULT 5
LOCUS BF914566 620 bp mRNA linear EST 18-JAN-2001
DEFINITION IL3-UT0114-011200-362-E06 UT0114 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF914566
VERSION BF914566.1 GI:12306024
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NITH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 620)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3ut2=IL3-UT0114-
011200-362-E06&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 619.
Location/Qualifiers
1. .620
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0114"
/dev_stage="Adult"
/note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 181 a 157 c 150 g 132 t
ORIGIN

Query Match 88.2%; Score 19.4; DB 12; Length 620;
Best Local Similarity 95.2%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTCTTTGGGACAGGAGCT 21
|||||
Db 73 GCTCTTTGGGACAGGAGCT 93

RESULT 6
LOCUS BQ221568 851 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7559207 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6046477
5', mRNA sequence.
ACCESSION BQ221568
VERSION BQ221568.1 GI:20402968
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NITH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Mon Apr 21 10:30:29 2003

us-09-270-437d-13.rst

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM13292 row: f column: 14
 High quality sequence stop: 637.

FEATURES

source
 1. .851
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6046477"
 /clone_lib="NIH MGC 72"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT5; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 229 a 234 c 231 g 157 t

ORIGIN

Query Match 88.2%; Score 19.4; DB 14; Length 851;
 Best Local Similarity 95.2%; Pred. No. 1.9e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAAGGT 21

Db 86 GCTCTTTGGGACAGGAAGGT 106

RESULT 7

BG481336 874 bp mRNA linear EST 21-MAR-2001
 LOCUS 602528680F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4652395 5',
 DEFINITION mRNA sequence.

ACCESSION BG481336.1 GI:13413615

VERSION EST.

KEYWORDS human.

SOURCE

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 874)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM1436 row: 0 column: 20
 High quality sequence stop: 688.

FEATURES

source
 1. .874
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4652395"
 /clone_lib="NIH MGC 21"
 /tissue_type="choriocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming.
 Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

240 a 230 c 250 g 154 t

ORIGIN

Query Match 88.2%; Score 19.4; DB 12; Length 874;
 Best Local Similarity 95.2%; Pred. No. 1.9e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAAGGT 21

Db 116 GCTCTTTGGGACAGGAAGGT 136

RESULT 8

BG748346 889 bp mRNA linear EST 15-MAY-2001
 LOCUS 602705902F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842553 5',
 DEFINITION mRNA sequence.

ACCESSION BG748346

VERSION EST.

KEYWORDS human.

SOURCE

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 889)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM1677 row: c column: 02
 High quality sequence stop: 773.

FEATURES

source
 1. .889
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4842553"
 /clone_lib="NIH_MGC_43"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 Note: this is a NIH MGC Library.

242 a 241 c 235 g 171 t

BASE COUNT

ORIGIN

Query Match 88.2%; Score 19.4; DB 12; Length 889;
 Best Local Similarity 95.2%; Pred. No. 1.9e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAAGGT 21

Db 62 GCTCTTTGGGACAGGAAGGT 82

RESULT 9

B1871125/c B1871125 264 bp mRNA linear EST 11-OCT-2001
 LOCUS 603395008F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5405040 5',
 DEFINITION mRNA sequence.

ACCESSION B1871125

VERSION B1871125.1 GI:16044798

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 264)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cyapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12032 row: p column: 01
High quality sequence start: 9
High quality sequence stop: 264.
Location/Qualifiers
1..264
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5405040"
/clone_lib="NIH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 87 a 82 c 48 g 47 t

ORIGIN

Query Match 85.5%; Score 18.8; DB 13; Length 264;
Best Local Similarity 90.9%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAAGTC 22
|||||
Db 223 GCTCTGTGGGGCAGGAAGTC 202
|||||

RESULT 10
BM484358
LOCUS 538191 MARC 2P1G Sus scrofa cDNA 5', mRNA linear EST 05-FEB-2002

DEFINITION BM484358

ACCESSION BM484358

VERSION BM484358.1 GI:18534686

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 309)

AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.,
and Keele, J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for

JOURNAL EST discovery in swine

COMMENT Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

BASE COUNT 87 a 82 c 48 g 47 t

ORIGIN

Query Match 85.5%; Score 18.8; DB 13; Length 264;
Best Local Similarity 90.9%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAAGTC 22
|||||
Db 223 GCTCTGTGGGGCAGGAAGTC 202
|||||

RESULT 10
BM484358
LOCUS 538191 MARC 2P1G Sus scrofa cDNA 5', mRNA linear EST 05-FEB-2002

DEFINITION BM484358

ACCESSION BM484358

VERSION BM484358.1 GI:18534686

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 309)

AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.,
and Keele, J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for

JOURNAL EST discovery in swine

COMMENT Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 3 row: M column: 20
Seq primer: ATTAGTGACACTATAG.

FEATURES
source
1..309
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 72 a 93 c 86 g 58 t

ORIGIN

Query Match 85.5%; Score 18.8; DB 13; Length 309;
Best Local Similarity 90.9%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCTCTTTGGGACAGGAAGTC 22
|||||
Db 184 GCTCTTTGAGGACTGGAAGTC 163
|||||

RESULT 11
BF189397/c
LOCUS 234957 MARC 2P1G Sus scrofa cDNA 5', mRNA linear EST 02-NOV-2000

DEFINITION BF189397

ACCESSION BF189397

VERSION BF189397.1 GI:11072766

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 373)

AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.,
and Keele, J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for

JOURNAL EST discovery in swine

COMMENT Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

BASE COUNT 91 a 100 c 106 g 76 t

ORIGIN

Query Match 85.5%; Score 18.8; DB 12; Length 373;

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tcb/bac_ends/mouse/bac_end_intro.html. Plate: 271 row: L column: 15
Seq primer: SP6
Class: BAC ends.

FEATURES

source
Location/Qualifiers
1. .680
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-271L15"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI; RPCI-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."
BASE COUNT 169 a 155 c 159 g 197 t
ORIGIN

Query Match 83.6%; Score 18.4; DB 17; Length 680;
Best Local Similarity 95.0%; Pred. No. 5.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CTCTTTGGGACAGGAAGT 21
|||||
Db 67 CTCTTTGGGACAGGAAGT 86
|||||

RESULT 15
BG480515
LOCUS
DEFINITION 602529520F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4652981 5',
mRNA sequence.
BG480515
ACCESSION BG480515.1 GI:13412705
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 856)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1438 row: h column: 06
High quality sequence stop: 661.
Location/Qualifiers
1. .856
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4652981"
/clone_lib="NIH_MGC_21"
/tissue_type="Choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp

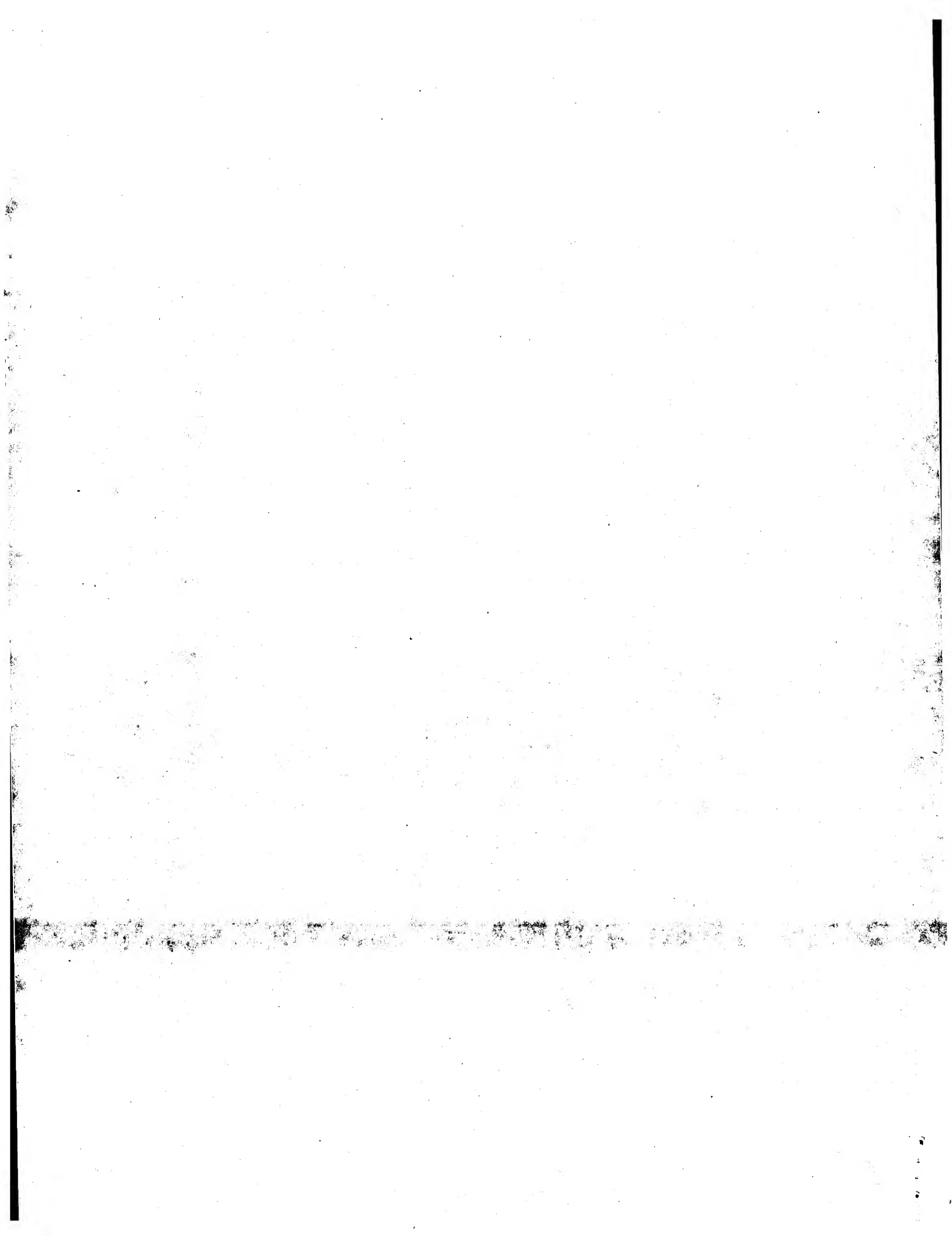
FEATURES

source
Location/Qualifiers
1. .856
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4652981"
/clone_lib="NIH_MGC_21"
/tissue_type="Choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 225 a 250 c 233 g 148 t
ORIGIN

Query Match 83.6%; Score 18.4; DB 12; Length 856;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCTCTTTGGGACAGGAAG 20
|||||
Db 117 GCTCTTTGGGACAGGAATG 136
|||||

Search completed: April 18, 2003, 07:32:01
Job time : 770.167 secs



GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:46:26 ; Search time 292 seconds
(without alignments)
2192.677 Million cell updates/sec

Title: US-09-270-437D-14
Perfect score: 22
Sequence: 1 gacgtgacacacggtttct 22
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.ey.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.nam.*
37: em.htg.vit.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	22	100.0	2010	9	AF117107	AF117107 Homo sapi
C 2	22	100.0	3283	6	ARI171867	ARI171867 Sequence
C 3	22	100.0	3412	6	ARI171865	ARI171865 Sequence
C 4	22	100.0	3642	9	BC021290	BC021290 Homo sapi
C 5	22	100.0	3667	9	AF057352	AF057352 Homo sapi
C 6	22	100.0	50320	2	AC126373	AC126373 Homo sapi
C 7	22	100.0	200947	2	AC016961	AC016961 Homo sapi
C 8	20.4	92.7	124849	2	AC094924	AC094924 Homo sapi
C 9	20.4	92.7	161691	2	AC126477	AC126477 Rattus no
C 10	18.8	85.5	91084	9	AL596177	AL596177 Human DNA
C 11	18.8	85.5	112259	2	AC026579	AC026579 Homo sapi
C 12	18.8	85.5	142971	9	AC020629	AC020629 Homo sapi
C 13	18.8	85.5	174623	2	AC108224	AC108224 Oryza sat
C 14	18.8	85.5	182695	2	AC015706	AC015706 Homo sapi
C 15	18.4	83.6	2219	1	NGU43735	U43735 Neisseria g
C 16	18.4	83.6	11099	1	AE002425	AE002425 Neisseria
C 17	18.4	83.6	11579	1	AE002453	AE002453 Neisseria
C 18	18.4	83.6	311321	1	NMA322491	AL162754 Neisseria
C 19	18.4	83.6	329861	1	NMA522491	AL162756 Neisseria
C 20	18.4	83.6	349980	6	AX044030	AX044030 Sequence
C 21	18.4	83.6	349980	6	AX044031	AX044031 Sequence
C 22	17.8	80.9	178212	2	AC107200	AC107200 Rattus no
C 23	17.4	79.1	4029	1	NMA277988	AJ277988 Natrialba
C 24	17.2	78.2	1929	14	AF121457	AF121457 Hyphantri
C 25	17.2	78.2	2341	1	RERORF1188	D30033 Rhodococcus
C 26	17.2	78.2	2809	8	TAU51304	U51304 Triticum ae
C 27	17.2	78.2	7001	1	AB016078	AB016078 Rhodococc
C 28	17.2	78.2	9515	1	AE007083	AE007083 Mycobacte
C 29	17.2	78.2	12948	1	AE006162	AE006162 Pasteurel
C 30	17.2	78.2	27548	1	HTCY27	295208 Mycobacteri
C 31	17.2	78.2	55380	8	NC21D9	295208 Mycobacteri
C 32	17.2	78.2	56510	2	AC020215	AL807373 Neurospor
C 33	17.2	78.2	62670	2	AC010566	AC020215 Drosophil
C 34	17.2	78.2	67375	2	AC104767	AC010566 Drosophil
C 35	17.2	78.2	67375	2	AC104767	AC104767 Homo sapi
C 36	17.2	78.2	79554	8	NCB11B23	AC104767 Homo sapi
C 37	17.2	78.2	113201	9	AP004290	AL669991 Neurospor
C 38	17.2	78.2	120524	9	AC008443	AP004290 Homo sapi
C 39	17.2	78.2	125798	9	AL390248	AC008443 Homo sapi
C 40	17.2	78.2	148824	2	AC025640	AL390248 Human DNA
C 41	17.2	78.2	151343	8	AC021893	AC025640 Homo sapi
C 42	17.2	78.2	159462	2	AC120991	AC021893 Genomic S
C 43	17.2	78.2	160930	9	AC010093	AC120991 Oryza sat
C 44	17.2	78.2	183455	2	AC008620	AC010093 Homo sapi
C 45	17.2	78.2	187226	9	AC104980	AC008620 Homo sapi
C 45	17.2	78.2	187226	9	AC104980	AC104980 Homo sapi

ALIGNMENTS

RESULT 1
AF117107/c
LOCUS AF117107
DEFINITION Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2) mRNA, complete cds.
ACCESSION AF117107
VERSION AF117107.1
KEYWORDS GI:4191609
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2010)
REFERENCE
Nielson, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H., Wewer, U.M. and Nielsen, F.C.
2010 bp mRNA linear PRI 26-JAN-1999

us-09-270-437d-14.rge

Mon Apr 21 10:30:32 2003

Query Match 100.0%; Score 22; DB 6; Length 3283;
 Best Local Similarity 100.0%; Pred. No. 9.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTTGACAAACGCGGTTTCT 22
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 Db 444 GAGCTTGACAAACGCGGTTTCT 423

RESULT 3
 LOCUS AR171865/c 3412 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 6 from patent US 6297364.
 ACCESSION AR171865
 VERSION AR171865.1 GI:17910815
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 3412)
 AUTHORS Chen, Y.-T., Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K.
 and Old, L.J.
 TITLE Isolated nucleic acid molecule encoding cancer associated antigen,
 the antigen itself, and uses thereof
 JOURNAL Patent: US 6297364-A 6 02-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..3412
 /organism="unknown"
 BASE COUNT 970 a 887 c 804 g 750 t 1 others
 ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 3412;
 Best Local Similarity 100.0%; Pred. No. 9.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTTGACAAACGCGGTTTCT 22
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 Db 444 GAGCTTGACAAACGCGGTTTCT 423

RESULT 4
 LOCUS BC021290/c 3642 bp mRNA linear PRI 22-JAN-2002
 DEFINITION Homo sapiens, IGF-II mRNA-binding protein 2, clone MGC:29539
 IMAGE:5090334, mRNA, complete cds.
 ACCESSION BC021290
 VERSION BC021290.1 GI:18204200
 KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 REFERENCE 1 (bases 1 to 3642)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (14-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
 COMMENT Contact: MGC help desk
 Email: gcapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 DNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc.mgc@nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,

A family of insulin-like growth factor II mRNA-binding proteins
 represses translation in late development
 Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
 99108099
 2 PUBMED
 2 (bases 1 to 2010)
 Nielsen, J., Christensen, J., Lykke-Andersen, J., Johnsen, A.H.,
 Wewer, U.M., and Nielsen, F.C.
 TITLE Direct Submission
 JOURNAL Submitted (30-DEC-1998) Institute of Molecular Biology, University
 of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
 FEATURES Location/Qualifiers
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 gene 1..2010
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 misc_feature 47
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 /note="alternative start-codon gives an additional
 N-terminal methionine"
 CDS 50..1846
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 SPSPQRAQRDHSRQGHAPGTSQARQIDFPLRLVPTQFVGLIISKEGLTIKNI
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 SAEIEMKGLBEAFENDMLAVQOANLIPGLNLSALGIFSTGLSVLSPGPRGAPPA
 APYHPTHTSGTFSLSLPHQFQFPFHHSVPQEIWNLFPIQAVGALIGKGAKIK
 QLAPFAGASIKIAPAEAGPDSERNVITGPEAQKQAGRIFGKLEENFNFKEBVK
 LEAHIRVPSSTGAVIGKGTNVLNLSAEVIVPRDPTDENEVIVRLIGHFFA
 SQAQRKIREIVQVQKQEQKYPQGVASQSRK"

BASE COUNT 565 a 552 c 532 g 361 t

ORIGIN

Query Match 100.0%; Score 22; DB 9; Length 2010;
 Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTTGACAAACGCGGTTTCT 22
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 Db 421 GAGCTTGACAAACGCGGTTTCT 400

RESULT 2
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 DEFINITION Sequence 8 from patent US 6297364.
 ACCESSION AR171867
 VERSION AR171867.1 GI:17910817
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 3283)
 AUTHORS Chen, Y.-T., Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K.
 and Old, L.J.
 TITLE Isolated nucleic acid molecule encoding cancer associated antigen,
 the antigen itself, and uses thereof
 JOURNAL Patent: US 6297364-A 8 02-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..3283
 /organism="unknown"
 BASE COUNT 945 a 833 c 779 g 725 t 1 others
 ORIGIN

Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tongson, E.E., Touchman, J.W., Tourgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, B.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAL Plate: 39 Row: 0 Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729883.

FEATURES

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1. .3667
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/db_xref="taxon:9606"
gene
1. .3667
/genes="p62"
436. .2106
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SAEIMKLEAFENDMLAVNQANLPLGLNSALGIFSTGLSVLSPAPRGPAPPA
APYHFTTSGTSSLYPHHGFPPPHHSYEQEIVNLFTPTQAVGAIIGKGAHTK
QARFAGASIKIAPAGDPVSRMVIITGPPEAQKQGRIFGKLKEENFNFKEVW
LEAHIRVPSSTAGRVIGKGTNVLNLSAEVIVPRDTPDENEIVRIIGHFPA
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BASE COUNT 1077 a 919 c 849 g 737 t

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SPSPQRAQRGDHSREGHAPGTSQARQIDFLRLVPTQFVGAIGKEGLTIKN
ITKQTSRVDIHRKNSGAEPVTHATPEGTSEACRMILIMQKEADETKLAEIPL
KLANGVLGRILGKGRNLKKIETHETGKTIISLQDLSIYNPRTITVKGTVAC
SAEIMKLEAFENDMLAVNQANLPLGLNSALGIFSTGLSVLSPAPRGPAPPA
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LEAHIRVPSSTAGRVIGKGTNVLNLSAEVIVPRDTPDENEIVRIIGHFPA
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BASE COUNT 1081 a 882 c 846 g 858 t

Query Match 100.0%; Score 22; DB 9; Length 3667;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGGCGGTTCT 22
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Db 810 GACGTTGACACGGCGGTTCT 789

RESULT 6

AC126373/c
LOCUS AC126373 50320 bp DNA linear HTG 05-JUL-2002
DEFINITION Homo sapiens chromosome 18 clone CTD-2307113 map 18, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC126373
VERSION AC126373.1 GI:21699324
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50320)
Birren, B., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone CTD-2307113
Unpublished

2 (bases 1 to 50320)
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgaltier, B.,
Camata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (05-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

TITLE

JOURNAL

RESULT 5

AF057352/c
LOCUS AF057352 3667 bp mRNA linear PRI 23-MAY-1999
DEFINITION Homo sapiens hepatocellular carcinoma autoantigen (p62) mRNA,
complete cds.
ACCESSION AF057352
VERSION AF057352.1 GI:4883680
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3667)
Zhang, J.Y., Chan, E.K., Peng, X.X. and Tan, E.M.

A novel cytoplasmic protein with RNA-binding motifs is an
autoantigen in human hepatocellular carcinoma
J. Exp. Med. 189 (7), 1101-1110 (1999)

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 3667)
Zhang, J.Y., Chan, E.K.L., Peng, X.X. and Tan, E.M.
Direct Submission
Submitted (03-APR-1998) Molecular & Experimental Medicine, The
Scripps Research Institute, 10550 N. Torrey Pines Road, La Jolla,
CA 92037, USA

Mon Apr 21 10:30:32 2003

COMMENT

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27661
Center clone name: 2307_I_13

NOTE: This record contains 59 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved. 766: contig of 766 bp in length

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* 767 866: gap of 100 bp
* 867 1574: contig of 708 bp in length
* 1575 1674: gap of 100 bp
* 1675 2412: contig of 738 bp in length
* 2413 2512: gap of 100 bp
* 2513 3283: contig of 771 bp in length
* 3284 3383: gap of 100 bp
* 3384 4124: contig of 741 bp in length
* 4125 4224: gap of 100 bp
* 4225 4938: contig of 714 bp in length
* 4939 5038: gap of 100 bp
* 5039 5920: contig of 782 bp in length
* 5921 6685: contig of 765 bp in length
* 6686 6785: gap of 100 bp
* 6786 7580: contig of 795 bp in length
* 7581 7680: gap of 100 bp
* 7681 8432: contig of 752 bp in length
* 8433 8532: gap of 100 bp
* 8533 9281: contig of 749 bp in length
* 9282 9381: gap of 100 bp
* 9382 10136: contig of 735 bp in length
* 10137 10236: gap of 100 bp
* 10237 10967: contig of 731 bp in length
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* 14366 14465: gap of 100 bp
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* 15204 15303: gap of 100 bp
* 15304 16010: contig of 707 bp in length
* 16011 16110: gap of 100 bp
* 16111 16872: contig of 762 bp in length
* 16873 16972: gap of 100 bp
* 16972 17715: contig of 743 bp in length
* 17716 17815: gap of 100 bp
* 17816 18587: contig of 772 bp in length
* 18588 18687: gap of 100 bp
* 18688 19464: contig of 777 bp in length
* 19465 19564: gap of 100 bp
* 19565 20303: contig of 739 bp in length
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* 20404 21135: contig of 732 bp in length
* 21136 21235: gap of 100 bp

FEATURES
source

Location/Qualifiers
1. 50320
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/db xref="taxon:9606"
/chromosome="18"
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* 22847 22946: gap of 100 bp
* 22947 23709: contig of 763 bp in length
* 23710 23809: gap of 100 bp
* 23810 24525: contig of 716 bp in length
* 24526 24625: gap of 100 bp
* 24626 25371: contig of 746 bp in length
* 25372 25471: gap of 100 bp
* 25472 26239: contig of 768 bp in length
* 26240 26339: gap of 100 bp
* 26340 27090: contig of 751 bp in length
* 27091 27190: gap of 100 bp
* 27191 27946: contig of 756 bp in length
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* 28047 28808: contig of 762 bp in length
* 28809 28908: gap of 100 bp
* 28909 29669: contig of 761 bp in length
* 29670 29769: gap of 100 bp
* 29770 30550: contig of 781 bp in length
* 30551 30650: gap of 100 bp
* 30651 31423: contig of 773 bp in length
* 31424 31523: gap of 100 bp
* 31524 32279: contig of 756 bp in length
* 32280 32379: gap of 100 bp
* 32380 33129: contig of 750 bp in length
* 33130 33229: gap of 100 bp
* 33230 33984: contig of 755 bp in length
* 33985 34084: gap of 100 bp
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* 34829 34928: gap of 100 bp
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* 35666 35765: gap of 100 bp
* 35766 36535: contig of 770 bp in length
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* 45159 45258: gap of 100 bp
* 45259 46040: contig of 782 bp in length
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* 46141 46894: contig of 754 bp in length
* 46895 46994: gap of 100 bp
* 46995 47754: contig of 760 bp in length
* 47755 47854: gap of 100 bp
* 47855 48596: contig of 742 bp in length
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
Db 567 GACGTTGACACGCGGTTTCT 546

RESULT 7
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LOCUS
DEFINITION Homo sapiens chromosome 3 clone RP11-394J21, WORKING DRAFT
ACCESSION AC016961
VERSION AC016961.27 GI:21908412
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEPIN.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 200947)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Albrow, S.L., Amarutunge, H.C., Are, J.R., Ayale, M., Banks, T.,
Barbata, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, S., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, I., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
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Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
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Karissone, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loubege, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okunolu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pichers, A., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojuben, I., Ruiz, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I.,
Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 200947)
Worley, K.C.
Direct Submission
Submitted (09-DEC-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Worley, K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 19, 2002 this sequence version replaced gi:21539678.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HMVB
Center clone name: RP11-394J21
----- Summary Statistics
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-terminator Big Dye: 98% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 200560 bases at least Q40
Consensus quality: 200582 bases at least Q30
Estimated insert size: 203982; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 13815: contig of 13815 bp in length
* 13816 13915: gap of unknown length
* 13916 200947: contig of 187032 bp in length.
FEATURES
Location/Qualifiers
1..200947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-394J21"
BASE COUNT 59914 a 43317 c 42497 g 55118 t 101 others
ORIGIN
Query Match 100.0%; Score 22; DB 2; Length 200947;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
Db 75177 GACGTTGACACGCGGTTTCT 75198

RESULT 8
AC094924/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-3M13, *** SEQUENCING IN PROGRESS ***,
48 unordered pieces.
ACCESSION AC094924
VERSION AC094924.3 GI:21716147
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 (bases 1 to 124849)
Muzay, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbara, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Briviera, M., Brown, E., Brown, M., Bryant, N.P., Buha, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carton, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delnathwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudan, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lien, C., Liu, J., Liu, W., Loulseged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sison, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

2 (bases 1 to 124849)
Unpublished
Worley, K.C.

Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 124849)
Worley, K.C.

Direct Submission
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 9, 2002 this sequence version replaced gi:17941723.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GBSF
Center Clone name: CH230-3M13
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 78224 bases at least Q40
Consensus quality: 82998 bases at least Q30
Consensus quality: 86973 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

1024: contig of 1024 bp in length
1124: gap of unknown length
1125: 2713: contig of 1589 bp in length
2714: 2813: gap of unknown length
2814: 4159: contig of 1346 bp in length
4160: 4259: gap of unknown length
4260: 5350: contig of 1091 bp in length
5351: 5450: gap of unknown length
5451: 6467: contig of 1017 bp in length
6468: 6567: gap of unknown length
6568: 7705: contig of 1138 bp in length
7706: 7805: gap of unknown length
7806: 8835: contig of 1030 bp in length
8836: 8935: contig of 1351 bp in length
8936: 10286: gap of unknown length
10287: 11667: contig of 1281 bp in length
11668: 11767: gap of unknown length
11768: 13491: contig of 1724 bp in length
13492: 13591: gap of unknown length
13592: 14980: contig of 1389 bp in length
14981: 15080: gap of unknown length
15081: 16363: contig of 1283 bp in length
16364: 16463: gap of unknown length
16464: 18175: contig of 1712 bp in length
18176: 18275: gap of unknown length
18276: 19880: contig of 1605 bp in length
19881: 19980: gap of unknown length
19981: 21031: contig of 1051 bp in length
21032: 21131: gap of unknown length
21132: 22509: contig of 1378 bp in length
22510: 22609: gap of unknown length
22610: 24990: contig of 2381 bp in length
24991: 25090: gap of unknown length
25091: 26426: contig of 1336 bp in length
26427: 26526: gap of unknown length
26527: 28449: contig of 1923 bp in length
28450: 28549: gap of unknown length
28550: 30854: contig of 2305 bp in length
30855: 30954: gap of unknown length
30955: 32874: contig of 1920 bp in length
32875: 32974: gap of unknown length
32975: 35321: contig of 2347 bp in length
35322: 35421: gap of unknown length
35422: 36868: contig of 1447 bp in length
36869: 36968: gap of unknown length
36969: 39827: contig of 2759 bp in length
39828: 39827: gap of unknown length
39828: 40925: contig of 1098 bp in length
40926: 41025: gap of unknown length
41026: 44017: contig of 2992 bp in length
44018: 44117: gap of unknown length
44118: 45537: contig of 1420 bp in length
45538: 45637: gap of unknown length
45638: 46742: contig of 1105 bp in length
46743: 46842: gap of unknown length
46843: 48312: contig of 1470 bp in length
48313: 48412: gap of unknown length
48413: 50676: contig of 2264 bp in length
50677: 50776: gap of unknown length
50777: 52607: contig of 1831 bp in length
52608: 52707: gap of unknown length
52708: 54385: contig of 1678 bp in length
54386: 54485: gap of unknown length

* 54486 58259: contig of 3774 bp in length
 * 58360 58359: gap of unknown length
 * 61228 61228: contig of 2869 bp in length
 * 61329 61329: gap of unknown length
 * 64029 64029: contig of 2701 bp in length
 * 64129 64129: gap of unknown length
 * 67245 67245: contig of 3116 bp in length
 * 67346 67346: gap of unknown length
 * 70188 70188: contig of 2843 bp in length
 * 70289 70289: gap of unknown length
 * 73912 73911: contig of 3623 bp in length
 * 74012 74011: gap of unknown length
 * 78471 78470: contig of 4459 bp in length
 * 78571 78570: gap of unknown length
 * 82831 82831: contig of 4261 bp in length
 * 82932 82931: gap of unknown length
 * 86896 86895: contig of 3964 bp in length
 * 86996 86996: gap of unknown length
 * 91367 91366: contig of 4371 bp in length
 * 91467 91466: gap of unknown length
 * 95237 95236: contig of 3770 bp in length
 * 95337 95336: gap of unknown length
 * 98741 98740: contig of 3404 bp in length
 * 98841 98840: gap of unknown length
 * 102541 102540: contig of 3700 bp in length
 * 102641 102640: gap of unknown length
 * 109458 109457: contig of 6817 bp in length
 * 109558 109557: gap of unknown length
 * 117663 117662: contig of 8105 bp in length
 * 117663 117662: gap of unknown length
 * 117663 124849: contig of 7087 bp in length.

FEATURES

Location/Qualifiers
 1..124849
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /clones="CH230-3M13"
 BASE COUNT 31267 a 26760 c 26699 g 30221 t 9902 others
 ORIGIN

Query Match 92.7%; Score 20.4; DB 2; Length 124849;
 Best Local Similarity 95.5%; Pred. No. 41;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GACGTTGACACGGCGGTTTCT 22
 |||||
 Db 36120 GACGTTGACACGGCGGTTTCT 36099

RESULT 9
 AC126477
 LOCUS
 DEFINITION Rattus norvegicus clone CH230-43M20, linear HTG 11-JUL-2002
 *** 62 unordered pieces.
 AC126477 161691 bp DNA HTG 11-JUL-2002
 AC126477 GI:21700419
 HTG; HTGS PHASE1.

ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 161691)

Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayelle,M., Banks,T.,
 Barbata,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buay,C., Burch,P., Burrett,C., Burrell,K.L., Byrd,N.C.,
 Carron,F.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

Barnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrall,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollings,B.,
 Homs,F., Howard,S., Huber,J., Huiyk,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
 Kratovic,J., Kureahi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louie,H.,
 Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
 Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
 Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzger,M.,
 Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
 Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
 Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,
 Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
 Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savary,G.,
 Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
 Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Tabof,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G. and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 161691)
 Worley,K.C.
 Direct Submission
 Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 161691)
 Worley,K.C.
 Direct Submission
 Submitted (11-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GFBV
 Center clone name: CH230-43M20
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 112006 bases at least Q40
 Consensus quality: 118246 bases at least Q30
 Consensus quality: 122772 bases at least Q20
 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 62 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1016: contig of 1016 bp in length
 * 1017 1116: gap of unknown length
 * 1117 2386: contig of 1170 bp in length
 * 2387 2386: gap of unknown length

73444: gap of unknown length
73445: contig of 3147 bp in length
76591: gap of unknown length
76592: contig of 2535 bp in length
76593: gap of unknown length
79227: contig of 3228 bp in length
82554: gap of unknown length
82555: contig of 3429 bp in length
86083: gap of unknown length
86084: contig of 2228 bp in length
86184: gap of unknown length
88511: contig of 2173 bp in length
90684: gap of unknown length
90784: contig of 2802 bp in length
93586: gap of unknown length
93587: contig of 3511 bp in length
93687: gap of unknown length
97198: contig of 2858 bp in length
100155: gap of unknown length
100156: gap of 3594 bp in length
100256: gap of unknown length
103849: contig of 3866 bp in length
103949: gap of unknown length
103950: contig of 5078 bp in length
107816: gap of unknown length
107915: gap of unknown length
112993: gap of 2469 bp in length
113094: gap of unknown length
115662: contig of 2463 bp in length
118125: gap of unknown length
118126: contig of 4073 bp in length
118226: gap of unknown length
122299: gap of unknown length

Query Match 92.7%; Score 20.4; DB 2; Length 161691;
Best Local Similarity 95.5%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACGTGACACGCGGTTCCT 22
DB 148271 GACGTGACACGCGGTTCCT 148292

RESULT 10
AL596177/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL596177
Human DNA sequence from clone RP11-325P15 on chromosome 1, complete
sequence.
AL596177
AL596177.4 GI:15552942
HTG.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91084)
Direct Submission
Submitted (08-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 11, 2001 this sequence version replaced gi:15022347.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e.: phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following

4099: contig of 1713 bp in length
4199: gap of unknown length
5288: contig of 1529 bp in length
5829: gap of unknown length
7407: contig of 1579 bp in length
7507: gap of unknown length
7508: contig of 1252 bp in length
8559: gap of unknown length
8760: contig of 1547 bp in length
8860: gap of unknown length
10407: contig of 1464 bp in length
11970: gap of unknown length
12070: gap of unknown length
13289: contig of 1219 bp in length
13399: gap of unknown length
14477: contig of 1088 bp in length
14577: gap of unknown length
15963: contig of 1386 bp in length
16063: gap of unknown length
16457: contig of 1394 bp in length
17557: gap of unknown length
19515: contig of 1958 bp in length
19615: gap of unknown length
20985: contig of 1370 bp in length
21085: gap of unknown length
23040: contig of 1955 bp in length
23140: gap of unknown length
25072: contig of 1932 bp in length
25172: gap of unknown length
28030: contig of 2858 bp in length
28130: gap of unknown length
30115: contig of 1985 bp in length
30215: gap of unknown length
31648: contig of 1433 bp in length
31749: gap of unknown length
33488: contig of 1640 bp in length
33489: gap of unknown length
33525: contig of 1764 bp in length
33526: gap of unknown length
36783: contig of 1431 bp in length
36883: gap of unknown length
37977: contig of 1094 bp in length
40083: contig of 2006 bp in length
40183: gap of unknown length
41999: contig of 1816 bp in length
42099: gap of unknown length
44664: contig of 2565 bp in length
44764: gap of unknown length
45960: contig of 1196 bp in length
46060: gap of unknown length
47229: contig of 1669 bp in length
47829: gap of unknown length
49786: contig of 1957 bp in length
49886: gap of unknown length
51125: contig of 1239 bp in length
51225: gap of unknown length
54559: contig of 3234 bp in length
54559: gap of unknown length
56015: contig of 1456 bp in length
56115: gap of unknown length
59017: contig of 2902 bp in length
59117: gap of unknown length
61064: contig of 1947 bp in length
61164: gap of unknown length
63433: contig of 2269 bp in length
63533: gap of unknown length
65766: contig of 2233 bp in length
65866: gap of unknown length
68115: contig of 2249 bp in length
68215: gap of unknown length
70969: contig of 2754 bp in length
71069: gap of unknown length
73344: contig of 2275 bp in length
71070

abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl>. RP11-325P15 is from the library RCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-325P15. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-325P15 is at 1 in this sequence. The true left end of clone RP11-337C18 is at 89085 in this sequence. The true right end of clone RP4-704D21 is at 41034 in this sequence.

```

FEATURES             Location/Qualifiers
     source            1..91084
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /clone="RP11-325P15"
                     /clone_lib="RCI-11.2"
BASE COUNT          27074 a 19586 c 19377 g 25047 t
ORIGIN

```

```

Query Match          85.5%; Score 18.8; DB 9; Length 91084;
Best Local Similarity 90.9%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 GACGTTGACACGCGGTTTCT 22
Db 9827 GACGTTGACACGCGGTTTCT 9806

```

```

RESULT 11
LOCUS               AC026579
DEFINITION          Homo sapiens chromosome 15 clone RP11-76D16 map 15, LOW-PASS
                     AC026579
ACCESSION           AC026579.2 GI:17048293
VERSION             HTG; HTGS PHASE0.
KEYWORDS            Homo sapiens.
SOURCE              Homo sapiens
ORGANISM            Homo sapiens
REFERENCE            Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,
                     Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, P.,
                     Boguslavskiy, L., Bouckgalter, B., Brown, A., Burkett, G.,
                     Campopiano, A., Castle, P., Choe, P., Colangelo, M., Collins, S.,
                     Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
                     Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
                     Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
                     Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
                     Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
                     Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
                     Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
                     McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
                     Melarim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
                     Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
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                     Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
                     Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
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REFERENCE            Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,
                     Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, P.,
                     Boguslavskiy, L., Bouckgalter, B., Brown, A., Burkett, G.,
                     Campopiano, A., Castle, P., Choe, P., Colangelo, M., Collins, S.,
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                     2 (bases 1 to 112259)

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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
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Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Subunion
Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 22, 2001 this sequence version replaced gi:7284066.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8359
Center clone name: 76_D_16

* NOTE: This record contains 139 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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1 715 814: gap of 100 bp
815 1541: contig of 727 bp in length
1542 1641: gap of 100 bp
1642 2329: contig of 688 bp in length
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2430 3143: contig of 714 bp in length
3144 3243: gap of 100 bp
3244 3955: contig of 712 bp in length
3956 4055: gap of 100 bp
4056 4726: contig of 671 bp in length
4727 4826: gap of 100 bp
4827 5533: contig of 707 bp in length
5534 5633: gap of 100 bp
5634 6329: contig of 696 bp in length
6330 7152: contig of 723 bp in length
7153 7252: gap of 100 bp
7253 7978: contig of 726 bp in length
7979 8078: gap of 100 bp
8079 8772: contig of 694 bp in length
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8873 9570: contig of 698 bp in length
9571 9670: gap of 100 bp
9671 10355: contig of 685 bp in length
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11163 11262: gap of 100 bp
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12063 12759: contig of 697 bp in length
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12860 13633: contig of 674 bp in length
13634 14355: contig of 722 bp in length
14356 14455: gap of 100 bp
14456 15160: contig of 705 bp in length
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15261 15972: contig of 712 bp in length
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 * 18473 19195: contig of 723 bp in length
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 * 22420 23122: contig of 703 bp in length
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 * 54438 55155: contig of 718 bp in length

Query Match 85.5%; Score 18.8; DB 2; Length 112259;
 Best Local Similarity 90.9%; Pred. No. 2.4e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GACGTTGACAAACGGCGTTTCT 22
 DB 77471 GACGTTGACAAACGGCGTCTCT 77492

RESULT 12

AC020629/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC020629 142971 bp DNA linear PRI 07-MAR-2002
 Homo sapiens 12q BAC RP11-76B16 (Roswell Park Cancer Institute
 Human BAC Library) complete sequence.

AC020629.6 GI:7656675
 Homo sapiens.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 142971)
 Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,
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 Weinstein, I.R., Williamson, A., Worley, K., Wren, J., Wrensford, G.,
 Xiang, A.M., Yang, R., Yu, W., Zhou, X., Kucheraipati, R., Nelson, D. and
 Gibbs, R.

Direct Submission

Unpublished

2 (bases 1 to 142971)

Worley, K.C.

Direct Submission

Submitted (07-JAN-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One

REFERENCE
AUTHORS
TITLE
JOURNAL

Baylor Plaza, Houston, TX 77030, USA
Worley, K.C.
Direct Submission
Submitted (27-APR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 142971)
Worley, K.C.
Direct Submission
Submitted (28-APR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 142971)
Worley, K.C.
Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 27, 2000 this sequence version replaced gi:7025656.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

Contig length: 142971
Phrap values in estimate: 140680
Average error rate (BCM-Phrap estimate): 0.000118703
Fraction of Phrap values less than 40 : 0.0433608
Number of consensus changing edits: 31
Number of N's in consensus : 0

----- Summary Statistics -----
Position Original+Context Edited+Context
11171 gctctctgga(n)caaaaaaaa gctctctgga(n)caaaaaaaa
12018 tatctatctg(n)ctatatctat tatctatctg(n)ctatatctat

----- Consensus changing edits -----

16604 tccactctaa(n) agttccattt
18385 tagtaaccac(n) tacattttta
21879 aaaaaaaa(n) aattaaaaa
21880 aaaaaaaa(n) nnttaaaaa
21881 aaaaaaaa(n) nnttaaacag
21906 cctaggtccc(n) ttaaaacag
22169 accagctgg(n) ctaaatgag
38915 ttacatctag(n) tctttgaaa
55675 actttgctc(n) aaaaaaaa
57658 gaccagctg(n) ccaacatggt
74371 ggtggggcc(n) ccgcccgcg
8021 taatgaggg(n) agaccatgg
88248 gcatggagc(n) agatcacacc
94121 ttgttcctga(n) gctctctgc
95230 gtcctgtgc(n) nnttgcttc
95231 catgtgnc(n) nnttgcttc
95232 atgtgtnn(n) ntgttcaac
104931 ttgttttag(n) acagacagg
118168 gccaggtct(n) ccaaatggt
120974 catctaaa(n) ananagaac
120976 tctcaaaa(n) anangaactc
120978 tcaaaaana(n) anagaactct
120980 aaaaana(n) gaactcttc
139505 ccagccatgg(n) gngggccac
139508 gccatggng(n) gggcactctg
139598 attaccatta(n) aataggtat
140104 accgtgcca(n) cagaatagaa
140149 tggacaatt(n) gataccaca

----- Distribution of Quality < 40 Bases -----

# bases	1000	900	800	700	600	500	400	300	200	100	0
	*	*	*	*	*	*	*	*	*	*	*

----- Phrap Value Range -----

5	10	15	20	25	30	35	40
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Version: 1.01 qxfo.
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/rpt_family="Tigger2a"
/rpt_family="MSTD"
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/db_xref="dbSTS:11453"
/standard_name="Cda0yb04"
/db_xref="GDB:446196"

FEATURES
source

JOURNAL

COMMENT

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 26, 2000 this sequence version replaced gi:6454072.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
 Center project name: L1382

----- Summary Statistics
 Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 141788 bases at least Q40

Consensus quality: 163541 bases at least Q30

Consensus quality: 174566 bases at least Q20

Insert size: 181000; agarose-fp

Insert size: 181095; sum-of-contigs

Quality coverage: 4.2 in Q20 bases; agarose-fp
 Quality coverage: 4.2 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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2036 2135: gap of 100 bp

2136 6069: contig of 3934 bp in length

6070 6169: gap of 100 bp

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10461 10560: gap of 100 bp

10561 14300: contig of 3740 bp in length

14301 14400: gap of 100 bp

14401 18480: contig of 4080 bp in length

18481 18580: gap of 100 bp

18581 23093: contig of 4513 bp in length

23094 23193: gap of 100 bp

23194 28213: contig of 5020 bp in length

28214 28313: gap of 100 bp

28314 32808: contig of 4495 bp in length

32809 32908: gap of 100 bp

32909 37000: contig of 4092 bp in length

37001 37100: gap of 100 bp

37101 45183: contig of 8083 bp in length

45184 45283: gap of 100 bp

45284 53421: contig of 8138 bp in length

53422 53521: gap of 100 bp

53522 64476: contig of 10955 bp in length

64477 64576: gap of 100 bp

64577 75144: contig of 10568 bp in length

75145 75244: gap of 100 bp

75245 93230: contig of 17986 bp in length

93231 93330: gap of 100 bp

93331 116951: contig of 23621 bp in length

116952 117051: gap of 100 bp

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Location/Qualifiers
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/chromosome="1"

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FEATURES

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Query Match 85.5%; Score 18.8; DB 2; Length 182695;
 Best Local Similarity 90.9%; Pred. No. 2.3e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACACGGCGTTTCT 22
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Db 19692 GACGTTGACACAGTGGTTCT 19671
 |||||

RESULT 15

NGU43735

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

AUTHORS

NGU43735 2219 bp DNA linear BCT 30-JAN-1996

Neisseria gonorrhoeae restriction/modification system, M.Ngov

cytosine methylase (dcmE) gene, complete cds, and R.Ngov

restriction endonuclease (dcrE) gene, partial cds.

U43735

U43735.1 GI:1165240

Neisseria gonorrhoeae strain=WR302.

Neisseria gonorrhoeae

Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;

Neisseria.

1 (bases 1 to 2219)

Stein,D.C., Gunn,J.S., Radlinska,M. and Piekawicz,A.

Restriction and modification systems of Neisseria gonorrhoeae

Gene 157 (1-2), 19-22 (1995)

95331562

7607490

REFERENCE 2 (bases 1 to 2219)

Stein,D.C.

Mon Apr 21 10:30:32 2003

Direct Submission
 TITLE Submitted (20-DEC-1995) Daniel C. Stein, Microbiology, Univ.
 JOURNAL Maryland, College Park, MD 20742, USA
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 /translation="MQQIKFIDLPFGMSGIRKGFQACRQKQSVACCVFTSRIKPAAL
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 KEFGIPQNRKRIYLTGSKSPDLSFSPKNIILSGLPSTSPFIKLLKKFP
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 NIQWLGWLRKEIEFDVSTNTQMPDPFNLKDRSRELLLEVAFNRNACPGFDIA
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 KKAWCIRKARVFGTA"
 741 a 427 c 476 g 575 t
 BASE COUNT
 ORIGIN

Query Match 83.6%; Score 18.4; DB 1; Length 2219;
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GACGTTGACAAACGGCGGTTT 20
 |||||
 Db 1503 GTGTTGACAAACGGCGGTTT 1522

Search completed: April 18, 2003, 06:31:06
 Job time : 501 secs

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:12:35 ; Search time 98 seconds
(without alignments)
505.551 Million cell updates/sec

Title: US-09-270-437D-14

Perfect score: 22

Sequence: 1 gacgtgacacggcggtttct 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002:*

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	21	PCR primer for DNA
C 2	22	100.0	424	21	Human colon cancer
C 3	22	100.0	2010	23	DNA encoding novel
C 4	22	100.0	3283	21	An alternative for
C 5	22	100.0	3412	21	DNA encoding cancer
C 6	22	100.0	3667	23	DNA encoding novel
C 7	22	100.0	3694	22	Human cDNA encoding
C 8	18.4	83.6	999	24	DNA polymerase III
C 9	18.4	83.6	999	24	DNA polymerase III

C 10	18.4	83.6	999	24	ABL87977	DNA polymerase III
C 11	18.4	83.6	999	24	ABL87978	DNA polymerase III
C 12	18.4	83.6	12893	21	AA81733	N. meningitidis pa
C 13	18.4	83.6	102634	21	AA81733	N. meningitidis pa
C 14	18.4	83.6	349980	21	AA81733	N. meningitidis pa
C 15	18.4	83.6	349980	21	AA81733	Neisseria meningit
C 16	18.4	83.6	1437668	21	AA81733	Neisseria meningit
C 17	17.2	78.2	140	22	ABA11525	N. meningitidis B
C 18	17.2	78.2	404	21	ABA11525	Human nervous syst
C 19	17.2	78.2	7330	23	ABL06499	Human secreted pro
C 20	17.2	78.2	10543	23	ABL06499	Drosophila melanog
C 21	17.2	78.2	349980	22	ABL06499	Drosophila melanog
C 22	17.2	78.2	3378	23	ABL20008	Pyrococcus abyssi
C 23	16.8	76.4	512	21	AAF12699	Drosophila melanog
C 24	16.8	76.4	969	21	AAF12699	Aspergillus oryzae
C 25	16.8	76.4	974	21	AAF12699	Arabidopsis thalia
C 26	16.2	73.6	264	21	AA81490	Arabidopsis thalia
C 27	16.2	73.6	294	21	AA81490	Arabidopsis thalia
C 28	16.2	73.6	525	20	ABN21924	Human ORFX polynuc
C 29	16.2	73.6	594	21	AA81490	Human ORFX polynuc
C 30	16.2	73.6	683	21	AA81490	Calcineurin regula
C 31	16.2	73.6	696	21	AA81490	Arabidopsis thalia
C 32	16.2	73.6	883	21	AA81490	Arabidopsis thalia
C 33	16.2	73.6	973	24	ABN21924	Arabidopsis thalia
C 34	16.2	73.6	1026	20	AA81490	Human ORFX polynuc
C 35	16.2	73.6	1026	20	AA81490	Bacillus lichenifo
C 36	16.2	73.6	1026	21	AA81490	B. subtilis pectat
C 37	16.2	73.6	1026	22	AA81490	B. licheniformis p
C 38	16.2	73.6	1035	24	ABK75359	DNA encoding the m
C 39	16.2	73.6	1157	18	AA75430	Bacillus lichenifo
C 40	16.2	73.6	1390	24	AA75430	Xanthomonas campe
C 41	16.2	73.6	6250	19	AAV58731	Human serine/threo
C 42	16.2	73.6	6250	19	AAV58731	Pyrolytrin gene
C 43	16.2	73.6	8931	21	AAA75307	DNA sequence of Ps
C 44	16.2	73.6	56050	23	AA81490	DNA sequence of Bu
C 45	16.2	73.6	56485	21	AAA81476	Propionibacterium
						N. meningitidis pa

ALIGNMENTS

RESULT 1
AAZ36160
ID AAZ36160 standard; DNA; 22 BP.

XX AAZ36160;

XX AAZ36160;

DT 11-FEB-2000 (first entry)

XX PCR primer for DNA encoding cancer associated antigen KOC-3.

XX Cancer associated antigen; KOC-1; cancer; vaccine; CT7; PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

FN WO9954738-A1.

XX 28-OCT-1999.

PF 16-MAR-1999; 99WO-US05766.

XX 17-APR-1998; 98US-0061709.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;

XX WFI; 2000-013284/01.

XX Nucleotides representing cancer-associated genes, used to develop

PT products for the diagnosis, monitoring and treatment of cancers

XX

xx The present invention describes a library of polynucleotides comprising
cc 1079 nucleotide sequences (given in AAH30067 to AAH31145). Also described
cc 1080 nucleotide sequences (given in AAH30067 to AAH31145) having at least 90% identity to
cc 1081 the isolated polynucleotide (I) having at least 90% identity to

CC quantitating a polypeptide in tissue, as molecular

CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2010 BP; 565 A; 552 C; 532 G; 361 T; 0 other;

Query Match 100.0%; Score 22; DB 23; Length 2010;
 Best Local Similarity 100.0%; Pred. No. 0.48; 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

QY 1 GACGTTGACAAACGGCGTTTCT 22
 |||||
 Db 421 GACGTTGACAAACGGCGTTTCT 400

RESULT 4

AAS236154/c
 ID AAZ36154 standard; DNA; 3283 BP.

XX AAZ36154;
 AC AAZ36154;

XX 11-FEB-2000 (first entry)

XX An alternative form of DNA encoding cancer associated antigen KOC-3.

XX Cancer associated antigen; KOC-3; cancer; vaccine; CT7; ss.

XX Homo sapiens.

XX WO9954738-A1.

XX 28-OCT-1999.

XX 16-MAR-1999; 99WO-US05766.

XX 17-APR-1998; 98US-0061709.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;
 WPI; 2000-013284/01.

XX Nucleotides representing cancer-associated genes, used to develop
 XX products for the diagnosis, monitoring and treatment of cancers

XX Claim 55; Page 42-43; 44pp; English.

XX The present sequence represents an alternative form of a cancer
 XX associated antigen gene designated KOC-3. The specification also
 XX describes a cancer associated antigen designated CT7. The CT7
 XX polynucleotide was isolated from SK-MEL-37 melanoma cells. The
 XX polypeptide has some homology with MAGE-10, limited to about 210 carboxy
 XX terminal amino acids. The amino terminal of the protein has a repetitive
 XX pattern, with repeats rich in serine, proline, glutamine and leucine,
 XX and an almost invariable core of the peptide given in AAY43877. The CT7
 XX polypeptide can be processed to peptides which provoke lysis by
 XX cytolytic T cells. The polynucleotides and polypeptides can be used for
 XX treating a cancerous condition and screening for or diagnosing cancerous
 XX conditions. The cancer associated antigens can be used as an immunogenic
 XX or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or
 XX granulocyte macrophage-colony stimulating factor (GM-CSF).

XX Sequence 3283 BP; 945 A; 833 C; 779 G; 725 T; 1 other;

Query Match 100.0%; Score 22; DB 21; Length 3283;
 Best Local Similarity 100.0%; Pred. No. 0.49; 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

QY 1 GACGTTGACAAACGGCGTTTCT 22
 |||||
 Db 444 GACGTTGACAAACGGCGTTTCT 423

RESULT 5

AAS36152/c
 ID AAZ36152 standard; DNA; 3412 BP.

XX AAZ36152;
 AC AAZ36152;

XX 11-FEB-2000 (first entry)

XX DNA encoding cancer associated antigen KOC-3.

XX Cancer associated antigen; KOC-3; cancer; vaccine; CT7; ss.

XX Homo sapiens.

XX WO9954738-A1.

XX 28-OCT-1999.

XX 16-MAR-1999; 99WO-US05766.

XX 17-APR-1998; 98US-0061709.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;
 WPI; 2000-013284/01.

XX Nucleotides representing cancer-associated genes, used to develop
 XX products for the diagnosis, monitoring and treatment of cancers

XX Claim 55; Page 41; 44pp; English.

XX The present sequence represents a cancer associated antigen gene
 XX designated KOC-3. The specification also describes a cancer associated
 XX antigen designated CT7. The CT7 polynucleotide was isolated from
 XX SK-MEL-37 melanoma cells. The polypeptide has some homology with
 XX MAGE-10, limited to about 210 carboxy terminal amino acids. The amino
 XX terminal of the protein has a repetitive pattern, with repeats rich in
 XX serine, proline, glutamine and leucine, and an almost invariable core of
 XX the peptide given in AAY43877. The CT7 polypeptide can be processed to
 XX peptides which provoke lysis by cytolytic T cells. The polynucleotides
 XX and polypeptides can be used for treating a cancerous condition and
 XX screening for or diagnosing cancerous conditions. The cancer associated
 XX antigens can be used as an immunogenic or vaccine composition with an
 XX adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony
 XX stimulating factor (GM-CSF).

XX Sequence 3412 BP; 970 A; 887 C; 804 G; 750 T; 1 other;

Query Match 100.0%; Score 22; DB 21; Length 3412;
 Best Local Similarity 100.0%; Pred. No. 0.49; 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

QY 1 GACGTTGACAAACGGCGTTTCT 22
 |||||
 Db 444 GACGTTGACAAACGGCGTTTCT 423

RESULT 6

AAS70982/c
 ID AAS70982 standard; cDNA; 3667 BP.

XX

us-09-270-437d-14.rng

Mon Apr 21 10:30:36 2003

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AC AAS70982;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #6786.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG06795.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1; SEQ ID No 6786; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 3667 BP; 1081 A; 882 C; 846 G; 858 T; 0 other;
XX
XX Query Match 100.0%; Score 22; DB 23; Length 3667;
XX Best Local Similarity 100.0%; Pred. No. 0.5;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GACGTTGACACGCGGTTTCT 22
XX |||||
XX Db 810 GACGTTGACACGCGGTTTCT 789
XX
XX RESULT 7
XX AAS26150/c
XX ID AAS26150 standard; cDNA; 3694 BP.
XX
XX AAS26150;
XX
XX
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PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234597.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0241826.
 PR 08-NOV-2000; 2000US-024617.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.

01-DEC-2000; 2000US-0250391.
 05-DEC-2000; 2000US-0251030.
 05-DEC-2000; 2000US-0251988.
 05-DEC-2000; 2000US-0256719.
 06-DEC-2000; 2000US-0251479.
 08-DEC-2000; 2000US-0251856.
 08-DEC-2000; 2000US-0251868.
 08-DEC-2000; 2000US-0251869.
 08-DEC-2000; 2000US-0251989.
 11-DEC-2000; 2000US-0251990.
 11-DEC-2000; 2000US-0254097.
 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-488783/53.
 P-PSDB; AAU16163.

New nucleic acid molecules encoding 461 human secreted proteins for
 diagnosing, preventing, treating or ameliorating medical conditions and
 used as food additives or preservatives -
 Claim 1; SEQ ID No 329; 980pp; English.

The invention relates to isolated nucleic acid molecules and their
 encoded secreted proteins. The nucleic acids and proteins are used to
 prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 rabbits, goats, horses, cats, dogs, chickens or sheep. They
 are also used in diagnosing a pathological condition or susceptibility
 to a pathological condition. Antibodies to the proteins can also
 be used in alleviating symptoms associated with the disorders and in
 diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
 immunosorbent assays (ELISA). Disorders which are diagnosed or treated
 include autoimmune diseases e.g. rheumatoid arthritis,
 hyperproliferative disorders e.g. neoplasms of the breast or liver,
 cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 e.g. cerebral ischaemia, angiodysplasia, nervous system disorders e.g.
 Alzheimer's disease, infections caused by bacteria, viruses and fungi
 and ocular disorders e.g. corneal infection, and many other
 disorders listed in the specification. The polypeptides can also
 be used to aid wound healing and epithelial cell proliferation, to
 prevent skin aging due to sunburn, to maintain organs before
 transplantation, for supporting cell culture of primary tissues, to
 regenerate tissues and in chemotaxis. The polypeptides can also be used
 as a food additive or preservative to increase or decrease storage
 capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 minerals, cofactors and other nutritional components. The present
 sequence encodes a novel secreted protein of the invention.

Query Match 100.0%; Score 22; DB 22; Length 3694;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGCGGCTTCT 22
 |||||
 Db 467 GACGTTGACACGCGGCTTCT 446

RESULT 8
 ABL87975/c
 ID ABL87975 standard; DNA; 999 BP.
 XX
 AC ABL87975;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:61.
 XX
 KW DNA polymerase III holoenzyme delta subunit; DNA polymerase III;
 KW DnaX; hola; holB; antibacterial; tuberculostatic; antileprotic;
 KW bacterial infection; DNA replication modulation; gene; ds.

XX OS Neisseria meningitidis.
 XX PN WO200206532-A1.
 XX PD 24-JAN-2002.
 XX PF 16-JUL-2001; 2001WO-US222395.
 XX PR 14-JUL-2000; 2000US-218246P.
 XX PR 28-MAR-2001; 2001US-0818780.
 XX PA (REPL-) REPLIDYNE INC.
 XX PI Bullard JJ, Janjic N, McHenry CS;
 XX PF WPI; 2002-164785/21.
 XX DR P-PSDB; ABB84744.
 XX CC Nucleic acid encoding a DNA polymerase III holoenzyme delta subunit
 XX CC from bacteria, useful for screening agents that modulate the subunit
 XX CC activity which is useful in the treatment of bacterial infections e.g.
 XX CC S. pyogenes and S. aureus -
 XX PS Disclosure; Page 282; 500pp; English.
 XX CC The present invention describes nucleic acid sequences encoding a DNA
 XX CC polymerase III holoenzyme delta subunit (I) from bacteria. (I) has
 XX CC antibacterial; tuberculostatic; antileprotic. Methods from the present
 XX CC invention can be used for screening for bacterial DNA polymerase
 XX CC holoenzyme delta subunit proteins and agents that modulate their
 XX CC activity. The agents are useful in the treatment of bacterial
 XX CC infections e.g. S. pyogenes, S. aureus, S. pneumoniae, Mycoplasma,
 XX CC Yersinia, Corynebacterium, Salmonella, Mycobacterium tuberculosis or
 XX CC M. leprae. The invention provides a convenient means of identifying
 XX CC compounds which modulate DNA replication in bacteria and therefore
 XX CC provide antibacterial targets, and which are also useful for
 XX CC amplification of DNA. ABL87935 to ABL88071 and ABB84724 to ABB84816
 XX CC represent sequences used in the exemplification of the present
 XX CC invention.
 XX SQ Sequence 999 BP; 219 A; 262 C; 328 G; 190 T; 0 other;
 Query Match 83.6%; Score 18.4; DB 24; Length 999;
 Best Local Similarity 95.0%; Pred. No. 25;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GACGTTGACACGGCGGTTT 20
 |||||
 DB 621 GACGTTGGCAACGGCGGTTT 602
 RESULT 9
 ABL87976/C
 ID ABL87976 standard; DNA; 999 BP.
 XX AC ABL87976;
 XX DT 16-MAY-2002 (first entry)
 XX DE DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:62.
 XX KW DNA polymerase III holoenzyme delta subunit; DNA polymerase III;
 XX KW DnaX; hola; hola; antibacterial; tuberculostatic; antileprotic;
 XX KW bacterial infection; DNA replication modulation; gene; ds.
 XX OS Neisseria meningitidis.
 XX PF WO200206532-A1.
 XX PD 24-JAN-2002.
 XX PF 16-JUL-2001; 2001WO-US222395.

XX PR 14-JUL-2000; 2000US-218246P.
 XX PR 28-MAR-2001; 2001US-0818780.
 XX PA (REPL-) REPLIDYNE INC.
 XX PI Bullard JJ, Janjic N, McHenry CS;
 XX PF WPI; 2002-164785/21.
 XX DR P-PSDB; ABB84744.
 XX CC Nucleic acid encoding a DNA polymerase III holoenzyme delta subunit
 XX CC from bacteria, useful for screening agents that modulate the subunit
 XX CC activity which is useful in the treatment of bacterial infections e.g.
 XX CC S. pyogenes and S. aureus -
 XX PS Disclosure; Page 283-284; 500pp; English.
 XX CC The present invention describes nucleic acid sequences encoding a DNA
 XX CC polymerase III holoenzyme delta subunit (I) from bacteria. (I) has
 XX CC antibacterial; tuberculostatic; antileprotic. Methods from the present
 XX CC invention can be used for screening for bacterial DNA polymerase
 XX CC holoenzyme delta subunit proteins and agents that modulate their
 XX CC activity. The agents are useful in the treatment of bacterial
 XX CC infections e.g. S. pyogenes, S. aureus, S. pneumoniae, Mycoplasma,
 XX CC Yersinia, Corynebacterium, Salmonella, Mycobacterium tuberculosis or
 XX CC M. leprae. The invention provides a convenient means of identifying
 XX CC compounds which modulate DNA replication in bacteria and therefore
 XX CC provide antibacterial targets, and which are also useful for
 XX CC amplification of DNA. ABL87935 to ABL88071 and ABB84724 to ABB84816
 XX CC represent sequences used in the exemplification of the present
 XX CC invention.
 XX SQ Sequence 999 BP; 219 A; 263 C; 327 G; 190 T; 0 other;
 Query Match 83.6%; Score 18.4; DB 24; Length 999;
 Best Local Similarity 95.0%; Pred. No. 25;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GACGTTGACACGGCGGTTT 20
 |||||
 DB 621 GACGTTGGCAACGGCGGTTT 602
 RESULT 10
 ABL87977/C
 ID ABL87977 standard; DNA; 999 BP.
 XX AC ABL87977;
 XX DT 16-MAY-2002 (first entry)
 XX DE DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:64.
 XX KW DNA polymerase III holoenzyme delta subunit; DNA polymerase III;
 XX KW DnaX; hola; hola; antibacterial; tuberculostatic; antileprotic;
 XX KW bacterial infection; DNA replication modulation; gene; ds.
 XX OS Neisseria meningitidis.
 XX PF WO200206532-A1.
 XX PD 24-JAN-2002.
 XX PF 16-JUL-2001; 2001WO-US222395.
 XX PR 14-JUL-2000; 2000US-218246P.
 XX PR 28-MAR-2001; 2001US-0818780.
 XX PA (REPL-) REPLIDYNE INC.
 XX PI Bullard JJ, Janjic N, McHenry CS;
 XX PF WPI; 2002-164785/21.
 XX DR P-PSDB; ABB84744.

DR WPI; 2002-164785/21.
 DR P-PSDB; ABB84745.
 XX
 PT Nucleic acid encoding a DNA polymerase III holoenzyme delta subunit
 PT from bacteria, useful for screening agents that modulate the subunit
 PT activity which is useful in the treatment of bacterial infections e.g.
 PT S. pyogenes and S. aureus -
 XX
 XX Disclosure; Fig 4U; 500pp; English.
 XX
 CC The present invention describes nucleic acid sequences encoding a DNA
 CC polymerase III holoenzyme delta subunit (I) from bacteria. (I) has
 CC antibacterial, tuberculostatic; antileprotic. Methods from the present
 CC invention can be used for screening for bacterial DNA polymerase
 CC holoenzyme delta subunit proteins and agents that modulate their
 CC activity. The agents are useful in the treatment of bacterial
 CC infections e.g. S. pyogenes, S. aureus, S. pneumoniae, Mycoplasma,
 CC Yersinia, Corynebacterium, Salmonella, Mycobacterium tuberculosis or
 CC M. leprae. The invention provides a convenient means of identifying
 CC compounds which modulate DNA replication in bacteria and therefore
 CC provide antibacterial targets, and which are also useful for
 CC amplification of DNA. ABL87935 to ABL88071 and ABB84724 to ABB84816
 CC represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 999 BP; 222 A; 260 C; 327 G; 190 T; 0 other;
 Query Match 83.6%; Score 18.4; DB 24; Length 999;
 Best Local Similarity 95.0%; Pred. No. 25;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GACGTTGACACGCGCGTTT 20
 Db 621 GACGTTGACACGCGCGTTT 602
 RESULT 11
 ABL87978/C
 ID ABL87978 standard; DNA; 999 BP.
 AC ABL87978;
 XX
 DT 16-MAY-2002 (first entry)
 DE DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:65.
 XX
 KW DNA polymerase III holoenzyme delta subunit; DNA polymerase III;
 KW DnaX; hoiA; holB; antibacterial; tuberculostatic; antileprotic;
 KW bacterial infection; DNA replication modulation; gene; ds.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO200206532-A1.
 XX
 PD 24-JAN-2002.
 XX
 PF 16-JUL-2001; 2001WO-US22395.
 XX
 PR 14-JUL-2000; 2000US-218246P.
 XX
 PR 28-MAR-2001; 2001US-0818780.
 XX
 PA (REPL-) REPLIDYNE INC.
 XX
 XX Bullard JJ, Janjic N, McHenry CS;
 PI WPI; 2002-164785/21.
 XX
 DR P-PSDB; ABB84745.
 DR
 XX Nucleic acid encoding a DNA polymerase III holoenzyme delta subunit
 PT from bacteria, useful for screening agents that modulate the subunit
 PT activity which is useful in the treatment of bacterial infections e.g.
 PT S. pyogenes and S. aureus -

PS Disclosure; Page 287-289; 500pp; English.
 XX
 CC The present invention describes nucleic acid sequences encoding a DNA
 CC polymerase III holoenzyme delta subunit (I) from bacteria. (I) has
 CC antibacterial, tuberculostatic; antileprotic. Methods from the present
 CC invention can be used for screening for bacterial DNA polymerase
 CC holoenzyme delta subunit proteins and agents that modulate their
 CC activity. The agents are useful in the treatment of bacterial
 CC infections e.g. S. pyogenes, S. aureus, S. pneumoniae, Mycoplasma,
 CC Yersinia, Corynebacterium, Salmonella, Mycobacterium tuberculosis or
 CC M. leprae. The invention provides a convenient means of identifying
 CC compounds which modulate DNA replication in bacteria and therefore
 CC provide antibacterial targets, and which are also useful for
 CC amplification of DNA. ABL87935 to ABL88071 and ABB84724 to ABB84816
 CC represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 999 BP; 222 A; 260 C; 327 G; 190 T; 0 other;
 Query Match 83.6%; Score 18.4; DB 24; Length 999;
 Best Local Similarity 95.0%; Pred. No. 25;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GACGTTGACACGCGCGTTT 20
 Db 621 GACGTTGACACGCGCGTTT 602
 RESULT 12
 AAA81733/C
 ID AAA81733 standard; DNA; 12893 BP.
 AC AAA81733;
 XX
 DT 04-DEC-2000 (first entry)
 DE N. meningitidis partial DNA sequence gnm_280 SEQ ID NO:280.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW Meningococcus B; MenB; ds.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO200022430-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US23573.
 XX
 PR 09-OCT-1998; 98US-0103794.
 PR 30-APR-1999; 99US-0132068.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
 PI Masighani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 PI Rappuoli R, Pizza M;
 XX
 DR WPI; 2000-318079/27.
 XX
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be
 PT used in the diagnosis and treatment of N. meningitidis infection and
 PT other Neisserial infections, for example, N.gonorrhoea -
 XX
 PS Claim 7; Page 1561-1565; 1760pp; English.
 XX
 CC The present invention describes methods of obtaining immunogenic
 CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
 CC represent specifically claimed Neisseria meningitidis genomic DNA
 CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
 CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
 CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the

CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
 CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
 CC sequences, which are all used in the exemplification of the present
 CC invention. The nucleic acid sequences, protein sequences, and antibodies
 CC against them, can be used as a medicament (or in the manufacture of a
 CC medicament) for treating, preventing or diagnosing infection due to
 CC Neisserial bacteria. For example, some of the identified proteins could
 CC be components of vaccines against Meningococcus B; against all serotypes;
 CC from the bacterium will also facilitate production of biological probes,
 CC particularly organism-specific probes. Attempts to make efficacious
 CC Meningococcus B vaccines have also been tried but none have successfully
 CC overcome antigenic variability. The provision of further, complete
 CC sequences may provide an opportunity to identify secreted or surface
 CC exposed proteins that may be presumed targets for the immune system and
 CC which are not antigenically variable or at least more conserved than
 CC other more variable regions.
 CC
 XX SQ Sequence 12893 BP; 2829 A; 3164 C; 3741 G; 3159 T; 0 other;

Query Match 83.6%; Score 18.4; DB 21; Length 12893;
 Best Local Similarity 95.0%; Pred. No. 29;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACGTTGACACGGCGGTTT 20
 DB 2453 GACGTTGACACGGCGGTTT 2434

RESULT 13
 AAA81464/c
 ID AAA81464 standard; DNA; 102634 BP.
 XX
 XX AAA81464;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 XX N. meningitidis partial DNA sequence gnm_12 SEQ ID NO:12.
 XX
 XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW Meningococcus B; MenB; ds.
 XX
 XX Neisseria meningitidis.
 OS
 XX WO200022430-A2.
 XX
 XX 20-APR-2000.
 XX
 XX 08-OCT-1999; 99WO-US23573.
 XX
 XX 09-OCT-1998; 98US-0103794.
 XX
 XX 30-APR-1999; 99US-0132068.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC, Scarlato V;
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Rappuoli R;
 PI Rappuoli R, Pizza M;
 XX
 XX WPI; 2000-318079/27.
 XX
 XX Isolated nucleotide sequences of Neisseria meningitidis which can be
 PT used in the diagnosis and treatment of N. meningitidis infection and
 PT other Neisserial infections, for example, N.gonorrhoea -
 XX
 XX Claim 7; Page 353-383; 1760pp; English.
 PS
 XX The present invention describes methods of obtaining immunogenic
 CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
 CC represent specifically claimed Neisseria meningitidis genomic DNA

CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
 CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
 CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
 CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
 CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
 CC sequences, which are all used in the exemplification of the present
 CC invention. The nucleic acid sequences, protein sequences, and antibodies
 CC against them, can be used as a medicament (or in the manufacture of a
 CC medicament) for treating, preventing or diagnosing infection due to
 CC Neisserial bacteria. For example, some of the identified proteins could
 CC be components of vaccines against Meningococcus B; against all serotypes;
 CC from the bacterium will also facilitate production of biological probes,
 CC particularly organism-specific probes. Attempts to make efficacious
 CC Meningococcus B vaccines have also been tried but none have successfully
 CC overcome antigenic variability. The provision of further, complete
 CC sequences may provide an opportunity to identify secreted or surface
 CC exposed proteins that may be presumed targets for the immune system and
 CC which are not antigenically variable or at least more conserved than
 CC other more variable regions.
 CC
 XX SQ Sequence 102634 BP; 23871 A; 24828 C; 27888 G; 26042 T; 5 other;

Query Match 83.6%; Score 18.4; DB 21; Length 102634;
 Best Local Similarity 95.0%; Pred. No. 33;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACGTTGACACGGCGGTTT 20
 DB 44045 GTCGTTGACACGGCGGTTT 44026

RESULT 14
 AAF21608/c
 ID AAF21608 standard; DNA; 349980 BP.
 XX
 XX AAF21608;
 XX
 XX 13-MAR-2001 (first entry)
 XX
 XX Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
 XX
 XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 KW ds.
 XX
 XX Neisseria meningitidis.
 OS
 XX WO2000066791-A1.
 XX
 XX 09-NOV-2000.
 XX
 XX 08-MAR-2000; 2000WO-US05928.
 XX
 XX 30-APR-1999; 99US-0132068.
 XX
 XX 08-OCT-1999; 99WO-US23573.
 XX
 XX 28-FEB-2000; 2000GB-0004695.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX (GENO-) INST GENOMIC RES.
 XX
 XX Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC, Masignani V;
 PI Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R;
 PI Frazer CM, Grandi G;
 XX
 XX WPI; 2000-647603/62.
 XX
 XX Neisseria meningitidis B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent Neisserial infections -
 XX
 XX Claim 7; Appendix A; 692pp; English.
 PS


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XX CC The present invention describes the full length genome of
CC Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607
CC to AAF21613 represent fragments of the NMB genomic sequence, as the
CC sequence was too long to go in a record on its own it was split into 8
CC sequences which overlap each other at the beginning and end of each
CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at
CC the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at
CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
CC Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to
CC AAF21606 represent PCR primers which are used in the exemplification of
CC the present invention. The NMB genome and fragments from it have
CC antibacterial activity, and can be used in vaccines and gene therapy.
CC Neisseria nucleic acids, proteins and/or antibodies which binds to the
CC proteins can be used in compositions for treating or preventing infection
CC due to Neisseria bacteria or as a diagnostic reagent for detecting the
CC presence of Neisseria bacteria or of antibodies raised to Neisseria
CC bacteria. Computers, computer memory, computer storage medium or computer
CC databases can be used in a search to identify open reading frames (ORFs)
CC or coding sequences within the NMB genome. The DNA sequences provide
CC further opportunities to find antigenic or immunogenic proteins which are
CC more effective in vaccines than the outer membrane proteins currently
CC used.
XX CC
SQ Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 other;

Query Match      83.6%; Score 18.4; DB 21; Length 349980;
Best Local Similarity 95.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGGTTT 20
    ||||| ||||| ||||| ||||| |||||
Db 140350 GACGTTGACACGCGGGTTT 140331

RESULT 15
AAF21609/c
ID AAF21609 standard; DNA; 349980 BP.
XX CC
AC AAF21609;
XX CC
DT 13-MAR-2001 (first entry)
XX CC
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.
XX CC
KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
KW ds.
XX CC
OS Neisseria meningitidis.
XX CC
PN WO200066791-A1.
XX CC
PD 09-NOV-2000.
XX CC
PF 08-MAR-2000; 2000WO-US05928.
XX CC
PR 30-APR-1999; 99US-0132068.
PR 08-OCT-1999; 99WO-US23573.
PR 28-FEB-2000; 2000GB-0004655.
XX CC
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX CC
PI Pizza M, Hickey B, Peterson J, Tettelin H, Venter JC, Massignani V;
PI Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R;
PI Frazer CM, Grandi G;
XX CC
DR WPI; 2000-647603/62.
XX CC
PT Neisseria meningitidis B full length genome sequence and open reading
PT frames are used to detect, treat and prevent Neisseria infections -
XX CC

```

PS Claim 7; Appendix A; 692pp; English.

XX CC The present invention describes the full length genome of
 CC Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607
 CC to AAF21613 represent fragments of the NMB genomic sequence, as the
 CC sequence was too long to go in a record on its own it was split into 8
 CC sequences which overlap each other at the beginning and end of each
 CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at
 CC the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at
 CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
 CC Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to
 CC AAF21606 represent PCR primers which are used in the exemplification of
 CC the present invention. The NMB genome and fragments from it have
 CC antibacterial activity, and can be used in vaccines and gene therapy.
 CC Neisseria nucleic acids, proteins and/or antibodies which binds to the
 CC proteins can be used in compositions for treating or preventing infection
 CC due to Neisseria bacteria or as a diagnostic reagent for detecting the
 CC presence of Neisseria bacteria or of antibodies raised to Neisseria
 CC bacteria. Computers, computer memory, computer storage medium or computer
 CC databases can be used in a search to identify open reading frames (ORFs)
 CC or coding sequences within the NMB genome. The DNA sequences provide
 CC further opportunities to find antigenic or immunogenic proteins which are
 CC more effective in vaccines than the outer membrane proteins currently
 CC used.

XX CC
 SQ Sequence 349980 BP; 81351 A; 86755 C; 95584 G; 86290 T; 0 other;

Query Match 83.6%; Score 18.4; DB 21; Length 349980;
 Best Local Similarity 95.0%; Pred. No. 36;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGGTTT 20

Db 147755 GTCGTTGACACGCGGGTTT 147736

Search completed: April 18, 2003, 05:48:05
 Job time : 251 secs

GenCore version 5.1.4.p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:53:41 / Search time 21.5 Seconds
(without alignments)
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Title: US-09-270-437D-14

Perfect score: 22
Sequence: 1 gacgttgacacggcggtttct 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgm2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgm2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgm2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	100.0	3283	4	US-09-061-709-8
C 2	22	100.0	3412	4	US-09-061-709-6
C 3	16.2	73.6	524	1	US-08-328-322-16
4	16.2	73.6	812	1	US-08-328-322-13
5	16.2	73.6	1026	3	US-09-073-684-1
6	16.2	73.6	1026	4	US-09-198-956-7
7	16.2	73.6	1026	4	US-09-198-955A-3
8	16.2	73.6	1026	4	US-09-395-858A-11
9	16.2	73.6	1026	4	US-09-546-500-1
10	16.2	73.6	1026	4	US-09-546-762-1
11	16.2	73.6	1026	4	US-09-694-531-3
12	16.2	73.6	1026	4	US-09-670-141-7
13	16.2	73.6	6250	1	US-08-729-214-23
14	16.2	73.6	6250	3	US-09-028-934-23
15	16.2	73.6	8931	3	US-09-028-934-28
16	15.8	71.8	537	4	US-08-836-500A-3
17	15.8	71.8	1007	4	US-08-836-500A-1
18	15.8	71.8	1008	3	US-08-721-979A-13
19	15.8	71.8	1008	4	US-09-654-289-13
20	15.6	70.9	831	4	US-08-998-416-290
21	15.6	70.9	1276	4	US-08-981-957D-12
C 22	15.6	70.9	3579	1	US-08-674-168-15
C 23	15.6	70.9	3579	3	US-08-985-908-18
C 24	15.6	70.9	3579	3	US-08-852-730-3
C 25	15.6	70.9	3579	4	US-08-985-916-10
C 26	15.6	70.9	4403765	4	US-09-103-840A-2
C 27	15.2	69.1	5134	2	US-08-635-121-1

C 28	15.2	69.1	6718	2	US-08-962-284-1	Sequence 1, Appli
29	15.2	69.1	10718	3	US-08-325-426B-1	Sequence 1, Appli
30	15.2	69.1	20235	1	US-07-642-734C-3	Sequence 3, Appli
31	15.2	69.1	20235	3	US-08-439-009A-3	Sequence 3, Appli
32	15	68.2	50	4	US-09-237-712-92	Sequence 92, Appli
33	15	68.2	397	4	US-09-237-712-1	Sequence 1, Appli
C 34	14.8	67.3	111282	4	US-09-754-250-3	Sequence 2, Appli
35	14.8	67.3	4403765	4	US-09-103-840A-2	Sequence 1, Appli
36	14.8	67.3	4411529	4	US-09-103-840A-1	Sequence 1, Appli
C 37	14.6	66.4	341	2	US-08-975-316-39	Sequence 39, Appli
C 38	14.6	66.4	341	4	US-09-615-192A-19	Sequence 39, Appli
C 39	14.6	66.4	409	2	US-08-975-316-41	Sequence 41, Appli
C 40	14.6	66.4	409	4	US-09-615-192A-41	Sequence 118, App
C 41	14.6	66.4	538	4	US-09-615-192A-118	Sequence 15, Appl
C 42	14.6	66.4	1155	2	US-08-169-948B-15	Sequence 15, Appl
C 43	14.6	66.4	1155	2	US-08-448-873-15	Sequence 15, Appl
C 44	14.6	66.4	1155	4	US-08-382-452D-15	Sequence 15, Appl
C 45	14.6	66.4	1401	4	US-08-952-457-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-061-709-8/c
; Sequence 8, Application US/09061709B
; Patent No. 6297364
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
; FILE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/061.709B
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 8
; LENGTH: 3283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-061-709-8

Query Match 100.0%; Score 22; DB 4; Length 3283;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GACGTTGACACGGCGGTTTCT 22
Db 444 GACGTTGACACGGCGGTTTCT 423

RESULT 2
US-09-061-709-6/c
; Sequence 6, Application US/09061709B
; Patent No. 6297364
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
; FILE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/061.709B

Mon Apr 21 10:30:38 2003

Db 307 GACATTGACACGAGCGGTTTC 327

RESULT 4
US-08-328-322-13
; Sequence 13, Application US/08328322
; Patent No. 5723436
; GENERAL INFORMATION:
; APPLICANT: Huang, Laiqiang
; APPLICANT: Cyert, Martha S.
; TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
; TITLE OF INVENTION: and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,322
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: P38,615
; REFERENCE/DOCKET NUMBER: 8600-0151.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: genomic DNA fragment containing full
; INDIVIDUAL ISOLATE: CNB1 coding sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 54..104
; NAME/KEY: CDS
; LOCATION: 181..652
; US-08-328-322-13

Query Match 73.6%; Score 16.2; DB 1; Length 812;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTC 21
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Db 436 GACATTGACACGAGCGGTTTC 456

RESULT 5
US-09-073-684-1
; Sequence 1, Application US/09073684
; Patent No. 6124127
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene No. 6124127boe
; APPLICANT: Sch lein, Martin
; APPLICANT: Lange, Niels Erik Krebs

;; TITLE OF INVENTION: No. 6124127el Pectate Lyase
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 6124127o No. 6124127disk of No. 6124127th America, Inc.
;; STREET: 405 Lexington Avenue
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10174
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/073,684
;; FILING DATE: 6-MAY-1998
;; CLASSIFICATION: 0506
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Carol E. Rozek
;; REGISTRATION NUMBER: 36,993
;; REFERENCE/DOCKET NUMBER: 5543.200-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-0123
;; TELEFAX: 212-878-9655
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1026 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-073-684-1

Query Match 73.6%; Score 16.2; DB 3; Length 1026;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGCGGTTTC 21
Db 51 GTCATTGACAGCGCGGTTTC 71

RESULT 6
US-09-198-956-7
; Sequence 7, Application US/09198956
; Patent No. 6165769
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schulein, Martin
; APPLICANT: Lange, Niels Erik K.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Schnorr, Kirk
; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
; FILE REFERENCE: 5377.200-US
; CURRENT APPLICATION NUMBER: US/09/198,956
; CURRENT FILING DATE: 1998-11-24
; EARLIER APPLICATION NUMBER: 1344/97
; EARLIER FILING DATE: 1997-11-24
; EARLIER APPLICATION NUMBER: 60/067,240
; EARLIER FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-198-956-7

Query Match 73.6%; Score 16.2; DB 4; Length 1026;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGCGGTTTC 21
Db 51 GTCATTGACAGCGCGGTTTC 71

RESULT 7
US-09-198-955A-3
; Sequence 3, Application US/09198955A
; Patent No. 6187580
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schulein, Martin
; APPLICANT: Lange, Niels E.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Moller, Soren
; APPLICANT: Glad, Sanne O. S.
; APPLICANT: Kauppinen, Markus S.
; APPLICANT: Schnorr, Kirk
; APPLICANT: Kongsbak, Lars
; TITLE OF INVENTION: No. 6187580el Pectate Lyases
; FILE REFERENCE: 5378.200-US
; CURRENT APPLICATION NUMBER: US/09/198,955A
; CURRENT FILING DATE: 1998-11-24
; PRIOR APPLICATION NUMBER: 1343/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 1344/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/067,249
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 60/067,240
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 09/073,684
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/184,217
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Bacillus licheniformis - ATCC 14580
US-09-198-955A-3

Query Match 73.6%; Score 16.2; DB 4; Length 1026;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGCGGTTTC 21
Db 51 GTCATTGACAGCGCGGTTTC 71

RESULT 8
US-09-395-858A-11
; Sequence 11, Application US/09395858A
; Patent No. 6242014
; GENERAL INFORMATION:
; APPLICANT: Feng Xu
; TITLE OF INVENTION: Methods For Using Pectate Lyases In
; FILE REFERENCE: 5670.200-US
; CURRENT APPLICATION NUMBER: US/09/395,858A
; CURRENT FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 09/156,298
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-395-858A-11

us-09-270-437d-14.rni

Mon Apr 21 10:30:38 2003

ADDRESSEE: No. 62845240 No. 6284524disk of No. 6284524th America, Inc.

STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,762
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/073,684
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Carol E. Rozek
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5543.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-546-762-1

Query Match 73.6%; Score 16.2; DB 4; Length 1026;

Best Local Similarity 85.7%; Pred. No. 36;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTC 21

Db 51 GTCATTGACACGCGGTTTC 71

RESULT 11

US-09-694-531-3

; Sequence 3, Application US/09694531

; Patent No. 6368843

; GENERAL INFORMATION:

; APPLICANT: Andersen, Lene N.

; APPLICANT: Schuelein, Martin

; APPLICANT: Lange, Niels E.

; APPLICANT: Bjornvad, Mads E.

; APPLICANT: Moller, Soren

; APPLICANT: Glad, Sanne O. S.

; APPLICANT: Kauppinen, Markus S.

; APPLICANT: Schnorr, Kirk

; APPLICANT: Kongsbak, Lars

; TITLE OF INVENTION: No. 6368843el Pectate Lyases

; FILE REFERENCE: 5378-200-US

; CURRENT APPLICATION NUMBER: US/09/694,531

; CURRENT FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 09/198,955

; PRIOR FILING DATE: 1998-11-24

; PRIOR APPLICATION NUMBER: 1343/97

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 1344/97

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/067,249

; PRIOR FILING DATE: 1997-12-02

; PRIOR APPLICATION NUMBER: 60/067,240

; PRIOR FILING DATE: 1997-12-02

; PRIOR APPLICATION NUMBER: 09/073,684

; PRIOR FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: 09/184,217

Query Match 73.6%; Score 16.2; DB 4; Length 1026;

Best Local Similarity 85.7%; Pred. No. 36;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTC 21

Db 51 GTCATTGACACGCGGTTTC 71

RESULT 9

US-09-546-500-1

; Sequence 1, Application US/09546500

; Patent No. 6280995

; GENERAL INFORMATION:

; APPLICANT: Andersen, Lene No. 6280995boe

; APPLICANT: Schuelein, Martin

; APPLICANT: Lange, Niels Erik Krebs

; TITLE OF INVENTION: No. 6280995el Pectate Lyases

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 62809950 No. 6280995disk of No. 6280995th America, Inc.

; STREET: 405 Lexington Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10174

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/546,500

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/073,684

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Carol E. Rozek

; REGISTRATION NUMBER: 36,993

; REFERENCE/DOCKET NUMBER: 5543.200-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1026 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-546-500-1

Query Match 73.6%; Score 16.2; DB 4; Length 1026;

Best Local Similarity 85.7%; Pred. No. 36;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTC 21

Db 51 GTCATTGACACGCGGTTTC 71

RESULT 10

US-09-546-762-1

; Sequence 1, Application US/09546762

; Patent No. 6284524

; GENERAL INFORMATION:

; APPLICANT: Andersen, Lene No. 6284524boe

; APPLICANT: Schuelein, Martin

; APPLICANT: Lange, Niels Erik Krebs

; TITLE OF INVENTION: No. 6284524el Pectate Lyases

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

;; PRIOR FILING DATE: 1998-11-02
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 1026
;; TYPE: DNA
;; ORGANISM: Bacillus licheniformis - ATCC 14580
US-09-694-531-3

Query Match 73.6%; Score 16.2; DB 4; Length 1026;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACGTTGACACGGCGGTTTC 21
DB 51 GTCATTGACACGGCGGTTTC 71

RESULT 12

US-09-670-141-7
; Sequence 7, Application US/09670141
; Patent No. 6429000

GENERAL INFORMATION:

;; APPLICANT: Andersen, Lene N.
;; APPLICANT: Schuelein, Martin
;; APPLICANT: Lange, Niels Erik K.
;; APPLICANT: Bjornvad, Mads E.
;; APPLICANT: Schnorr, Kirk

;; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus

;; FILE REFERENCE: 5377-200-US

;; CURRENT APPLICATION NUMBER: US/09/670,141

;; CURRENT FILING DATE: 2000-09-26

;; PRIOR APPLICATION NUMBER: 09/198,956

;; PRIOR FILING DATE: 1998-11-24

;; PRIOR APPLICATION NUMBER: 1344/97

;; PRIOR FILING DATE: 1997-11-24

;; PRIOR APPLICATION NUMBER: 60/067,240

;; PRIOR FILING DATE: 1997-12-02

;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 7

;; LENGTH: 1026

;; TYPE: DNA

;; ORGANISM: Bacillus licheniformis

US-09-670-141-7

Query Match 73.6%; Score 16.2; DB 4; Length 1026;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACGTTGACACGGCGGTTTC 21
DB 51 GTCATTGACACGGCGGTTTC 71

RESULT 13

US-08-729-214-23

;; Sequence 23, Application US/08729214
;; Patent No. 5817502

GENERAL INFORMATION:

;; APPLICANT: Ligon, James M.

;; APPLICANT: Hill, Dwight Steven

;; APPLICANT: Ryals, John Andrew

;; APPLICANT: Hammer, Phillip E.

;; APPLICANT: van Pee, Karl-Heinz

;; APPLICANT: Kirner, Sabine

;; TITLE OF INVENTION: Genes for the synthesis of

;; TITLE OF INVENTION: antipathogenic substances

;; NUMBER OF SEQUENCES: 27

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Ciba-Geigy Corporation

;; STREET: 520 White Plains Road

;; CITY: Tarrytown
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10591
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/729,214
;; FILING DATE: TEA
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meigs, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: CGC 1506/CIPS
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 919-541-8587
;; TELEFAX: 919-541-8689
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6250 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 615..2228

;; OTHER INFORMATION: /label= ORF1

;; OTHER INFORMATION: /note= "Open Reading Frame #1 of DNA sequence"

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 2231..3313

;; OTHER INFORMATION: /label= ORF2

;; OTHER INFORMATION: /note= "Open Reading Frame #2 of DNA sequence"

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 3368..5065

;; OTHER INFORMATION: /label= ORF3

;; OTHER INFORMATION: /note= "Open Reading Frame #3 of DNA sequence"

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 5093..6202

;; OTHER INFORMATION: /label= ORF4

;; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence"

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 5093..6202

;; OTHER INFORMATION: /label= ORF4

;; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence"

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;; NAME/KEY: CDS

;; LOCATION: 5093..6202

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;; NAME/KEY: CDS

;; LOCATION: 5093..6202

;; OTHER INFORMATION: /label= ORF4

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;; NAME/KEY: CDS

;; LOCATION: 5093..6202

;; OTHER INFORMATION: /label= ORF4

;; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence"

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 5093..6202

;; OTHER INFORMATION: /label= ORF4

;; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence"

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 5093..6202

;; OTHER INFORMATION: /label= ORF4

;; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence"

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 5093..6202

;; OTHER INFORMATION: /label= ORF4

;; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence"

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 5093..6202

;; OTHER INFORMATION: /label= ORF4

;; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence"

;; FEATURE:

Query Match	Score 16.2;	DB 3;	Length 6250;
Best Local Similarity	73.6%;		
Pred. No. 46;			
85.7%;			
Mismatches	0;		
Indels	0;		
Gaps	0;		

Query Match 73.6%; Score 16.2; DB 3; Length 8931;
Best Local Similarity 85.7%; Pred. No. 48;
0. Mismatches 3; Indels 0
Conservative 48

RESULT 15
US-09-028-934-28
; Sequence 28, Application US/09028934
; Patent No. 6117670
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Lam, Steven T.

QY 1 GACGTTGACAAACGGCGGTTC 21
|||||
Db 5613 GACGTCGACAAACGGCGACTTC 5633

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 06:35:31 ; Search time 91.3333 Seconds
(without alignments)
241.975 Million cell updates/sec

Title: US-09-270-437D-14

Perfect score: 22

Sequence: 1 gacgttgacacggcggtttct 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 639749 seqs, 502280978 residues

Total number of hits satisfying chosen parameters: 1279498

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	22	100.0	3412	10	US-09-899-651-6
C 3	22	100.0	3694	10	US-09-764-864-329
C 4	16.8	76.4	369	10	US-09-924-035A-3
C 5	16.8	76.4	486	9	US-09-938-842A-689
C 6	16.2	73.6	1026	12	US-10-072-152-3
C 7	16.2	73.6	1035	10	US-09-974-300-2650
C 8	16.2	73.6	1653	9	US-09-906-419-28
C 9	15.8	71.8	1035	9	US-10-169-953-1
C 10	15.8	71.8	1279	9	US-09-813-153-59
C 11	15.8	71.8	1462	9	US-09-764-824-516
C 12	15.8	71.8	1842	9	US-09-938-842A-1028
C 13	15.8	71.8	3057	10	US-09-974-300-2660
C 14	15.6	70.9	411	10	US-09-960-352-11807
C 15	15.6	70.9	439	10	US-09-867-701-568
C 16	15.6	70.9	531	9	US-09-738-626-1202
C 17	15.6	70.9	1276	9	US-09-982-704-12
C 18	15.6	70.9	1287	12	US-10-062-254-243
C 19	15.6	70.9	1335	9	US-09-738-626-3451

C 20	15.6	70.9	1338	9	US-10-067-974-11
C 21	15.6	70.9	1400	9	US-09-746-660A-43
C 22	15.6	70.9	1596	9	US-09-938-842A-785
C 23	15.6	70.9	3579	9	US-10-226-136-18
C 24	15.6	70.9	3309400	9	US-09-738-626-1
C 25	15.4	70.0	222	10	US-09-974-300-4137
C 26	15.2	69.1	266	10	US-09-878-574-7377
C 27	15.2	69.1	696	9	US-09-738-626-581
C 28	15.2	69.1	1176	10	US-09-974-300-1080
C 29	15.2	69.1	1330	10	US-09-974-300-2336
C 30	15.2	69.1	3798	10	US-09-974-300-2175
C 31	15.2	69.1	3798	10	US-09-974-300-2193
C 32	15.2	69.1	5134	9	US-09-902-432-1
C 33	15.2	69.1	6160	9	US-09-902-432-3
C 34	15.2	69.1	12860	10	US-09-070-927A-144
C 35	15.2	69.1	33023	10	US-09-880-107-3350
C 36	14.8	67.3	315	9	US-09-738-626-3285
C 37	14.8	67.3	555	10	US-09-974-300-5604
C 38	14.8	67.3	633	10	US-09-974-300-1122
C 39	14.8	67.3	944	10	US-09-770-445-351
C 40	14.8	67.3	1257	9	US-09-738-626-3137
C 41	14.8	67.3	1971	10	US-09-974-300-322
C 42	14.8	67.3	3044	9	US-09-927-827-32
C 43	14.8	67.3	111282	12	US-10-094-989-3
C 44	14.8	67.3	3309400	9	US-09-738-626-1
C 45	14.6	66.4	222	10	US-09-770-696-20

ALIGNMENTS

RESULT 1
US-09-899-651-8/c
; Sequence 8, Application US/09899651
; Patent No. US20020111470A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseung
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/899,651
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 8
; LENGTH: 3283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-8

Query Match 100.0%; Score 22; DB 10; Length 3283;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GACGTTGACACGGCGGTTTCT 22
Db 444 GACGTTGACACGGCGGTTTCT 423

RESULT 2
US-09-899-651-6/c
; Sequence 6, Application US/09899651
; Patent No. US20020111470A1
; GENERAL INFORMATION:

; CURRENT APPLICATION NUMBER: US/10/072,152
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US/09/198,955
; PRIOR FILING DATE: 1998-11-24
; PRIOR APPLICATION NUMBER: 1343/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 1344/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/067,249
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 60/067,240
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 09/073,684
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/184,217
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Bacillus licheniformis - ATCC 14580
US-10-072-152-3

Query Match 73.6%; Score 16.2; DB 12; Length 1026;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGGCGGTTTC 21
Db 51 GTCATTGACACGGCGGTTTC 71

RESULT 7

US-09-974-300-2650
; Sequence 2650, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085,500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2650
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2650

Query Match 73.6%; Score 16.2; DB 10; Length 1035;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGGCGGTTTC 21
Db 62 GTCATTGACACGGCGGTTTC 82

RESULT 8

US-09-906-419-28/c
; Sequence 28, Application US/09906419
; Publication No. US20030037357A1
; GENERAL INFORMATION:
; APPLICANT: Shockey, Jay
; APPLICANT: Schnurr, Judy

; APPLICANT: Browse, John
; TITLE OF INVENTION: Plant Acyl-CoA Synthetases
; FILE REFERENCE: DOW-04679
; CURRENT APPLICATION NUMBER: US/09/906,419
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/220,474
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1653
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-906-419-28

Query Match 73.6%; Score 16.2; DB 9; Length 1653;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGGCGGTTTC 21
Db 1014 GACGATTACACGGCGGTTTC 994

RESULT 9

US-10-169-953-1
; Sequence 1, Application US/10169953
; Publication No. US2003004915A1
; GENERAL INFORMATION:
; APPLICANT: Thierry BAUSSANT
; APPLICANT: Pascale JEANNIN
; APPLICANT: Yves DELNESTE
; APPLICANT: Francois LAMNY
; APPLICANT: Jean-Yves BONNEFOY
; TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT
; TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT
; FILE REFERENCE: D18390
; CURRENT APPLICATION NUMBER: US/10/169,953
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: FR 00 00070
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1032)
; FEATURE:
; OTHER INFORMATION: p40
US-10-169-953-1

Query Match 71.8%; Score 15.8; DB 9; Length 1035;
Best Local Similarity 89.5%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGTTGACACGGCGGTTTC 21
Db 240 CGTTGACACGGCGGTTTC 258

RESULT 10

US-09-813-153-59
; Sequence 59, Application US/09813153
; Publication No. US20030045459A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023
; CURRENT APPLICATION NUMBER: US/09/813,153
; CURRENT FILING DATE: 2001-03-21

us-09-270-437d-14.rnpb

Mon Apr 21 10:30:40 2003

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; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1028
; LENGTH: 1842
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1028

Query Match          71.8%; Score 15.8; DB 9; Length 1842;
Best Local Similarity 89.5%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTT 19
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Db 1780 GACGATGACACGCGGTT 1798

RESULT 13
US-09-974-300-2660/c
; Sequence 2660, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Id Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085-500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2660
; LENGTH: 3057
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2660

Query Match          71.8%; Score 15.8; DB 10; Length 3057;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGTTGACACGCGGTTTC 21
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Db 172 CATTGACACGCGGATTTC 154

RESULT 14
US-09-960-352-11807
; Sequence 11807, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Ningbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511_006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24

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; PRIOR APPLICATION NUMBER: US/09/363,044
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
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; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-153-59

Query Match          71.8%; Score 15.8; DB 9; Length 1279;
Best Local Similarity 89.5%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGTTGACACGCGGTTT 20
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Db 815 ACGATGACATGCGGTTT 833

RESULT 11
US-09-764-872-516
; Sequence 516, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAL25
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 516
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-516

Query Match          71.8%; Score 15.8; DB 9; Length 1462;
Best Local Similarity 89.5%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACGTTGACACGCGGTTT 20
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Db 740 ATGATGACACGCGGTTT 758

RESULT 12
US-09-938-842A-1028
; Sequence 1028, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

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; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11807
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 50-LIB34-083-Q1-E1-E6
US-09-960-352-11807
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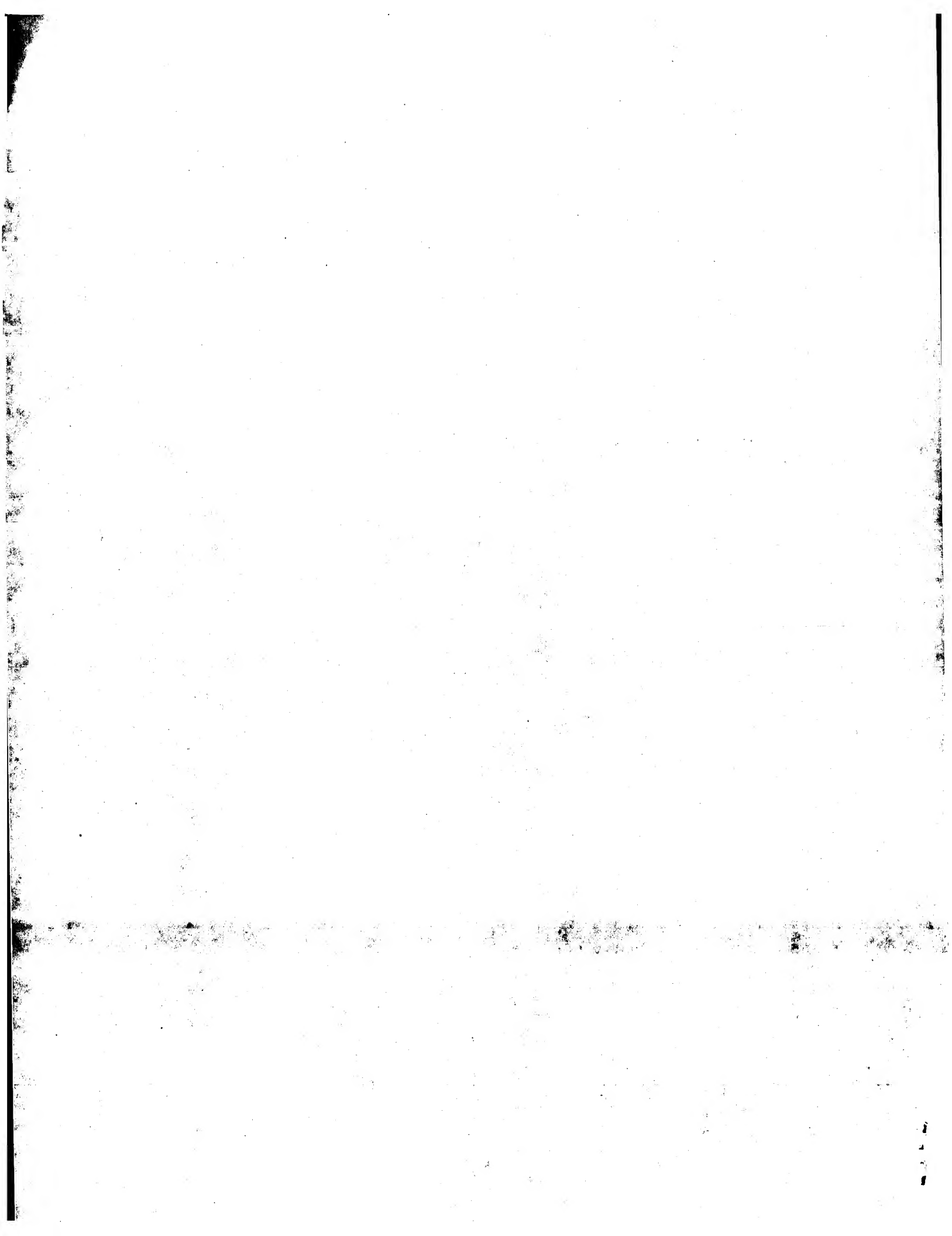
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; Sequence 568, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 568
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapien
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-568
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Best Local Similarity 81.8%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 26 GACATTGAGAACACGAGTTTCT 5
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Mon Apr 21 10:30:38 2003

us-09-270-437d-14.rni

Page 7

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GenCore version 5.1.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

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C 5	22	100.0	349	35	US-09-939-397-12874
C 6	22	100.0	363	16	US-09-289-768-32161
C 7	22	100.0	363	35	US-09-939-397-32161
C 8	22	100.0	409	25	US-09-652-918-3592
C 9	22	100.0	465	17	US-09-304-649-680
C 10	22	100.0	465	32	US-09-840-424-680
C 11	22	100.0	467	19	US-09-528-409-49810
C 12	22	100.0	467	35	US-09-933-524-49810
C 13	22	100.0	467	35	US-09-933-524-49810
C 14	22	100.0	546	56	US-60-125-787-430
C 15	22	100.0	2010	1	PCT-US01-08631-6785
C 16	22	100.0	3283	16	US-09-270-437-8
C 17	22	100.0	3283	33	US-09-899-651-8
C 18	22	100.0	3374	1	PCT-US01-01307-113
C 19	22	100.0	3374	39	US-10-092-302-113
C 20	22	100.0	3412	16	US-09-270-437-6
C 21	22	100.0	3412	33	US-09-899-651-6
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83: /cgn2_6/ptodata/1/pna/US6039 COMB.seq.*
84: /cgn2_6/ptodata/1/pna/US6040 COMB.seq.*
85: /cgn2_6/ptodata/1/pna/US6041 COMB.seq.*


```
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(347)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-121-1684

Query Match      100.0%; Score 22; DB 25; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACAAACGGCGGTTTCT 22
Db 323 GACGTTGACAAACGGCGGTTTCT 302

RESULT 4
US-09-289-768-12874/c
; Sequence 12874, Application US/09289768
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/289,768
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 39996
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12874
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(349)
; OTHER INFORMATION: n = A,T,C or G
US-09-289-768-12874

Query Match      100.0%; Score 22; DB 16; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACAAACGGCGGTTTCT 22
Db 122 GACGTTGACAAACGGCGGTTTCT 101

RESULT 5
US-09-939-397-12874/c
; Sequence 12874, Application US/09939397
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/939,397
; CURRENT FILING DATE: 2001-08-24
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 39996
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12874
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(349)
; OTHER INFORMATION: n = A,T,C or G
US-09-939-397-12874

Query Match      100.0%; Score 22; DB 35; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GACGTTGACAAACGGCGGTTTCT 22
Db 122 GACGTTGACAAACGGCGGTTTCT 101
```

```
RESULT 6
US-09-289-768-32161/c
; Sequence 32161, Application US/09289768
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/289,768
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 39996
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32161
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-289-768-32161
```

```
Query Match      100.0%; Score 22; DB 16; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GACGTTGACAAACGGCGGTTTCT 22
Db 276 GACGTTGACAAACGGCGGTTTCT 255
```

```
RESULT 7
US-09-939-397-32161/c
; Sequence 32161, Application US/09939397
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/939,397
; CURRENT FILING DATE: 2001-08-24
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 39996
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32161
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-939-397-32161
```

```
Query Match      100.0%; Score 22; DB 35; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GACGTTGACAAACGGCGGTTTCT 22
Db 276 GACGTTGACAAACGGCGGTTTCT 255
```

```
RESULT 8
US-09-652-918-3592/c
; Sequence 3592, Application US/09652918
; GENERAL INFORMATION:
; APPLICANT: Galvin, Katherine
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1187-001
; CURRENT APPLICATION NUMBER: US/09/652,918
; CURRENT FILING DATE: 2000-08-30
```

```

; PRIOR APPLICATION NUMBER: 60/151,130
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 8985
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3592
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(409)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-918-3592

Query Match      100.0%; Score 22; DB 25; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.7; 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY      1 GACGTTGACAAACGGCGGTTTCT-22
          |||||
DB      262 GACGTTGACAAACGGCGGTTTCT 241

RESULT 9
US-09-304-649-680/c
; Sequence 680, Application US/09304649
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN MICROVASCULAR ENDOTHELIAL LIBRARY
; FILE REFERENCE: MLN98-10PM
; CURRENT APPLICATION NUMBER: US/09/304,649
; CURRENT FILING DATE: 1999-05-04
; EARLIER APPLICATION NUMBER: 60/084,098
; EARLIER FILING DATE: 1998-05-04
; EARLIER APPLICATION NUMBER: 60/123,523
; EARLIER FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 60/126,974
; EARLIER FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 1311
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 680
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-304-649-680

Query Match      100.0%; Score 22; DB 17; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.7; 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY      1 GACGTTGACAAACGGCGGTTTCT 22
          |||||
DB      464 GACGTTGACAAACGGCGGTTTCT 443

RESULT 10
US-09-840-424-680/c
; Sequence 680, Application US/09840424
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN MICROVASCULAR ENDOTHELIAL LIBRARY
; FILE REFERENCE: 1600.1010-002
; CURRENT APPLICATION NUMBER: US/09/840,424
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/084,098

```

APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/933,524
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 09/528,409
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: HY-patent.pl Version 3.1
SEQ ID NO 49810
LENGTH: 467
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(467)
OTHER INFORMATION: n = A,T,C or G
US-09-933-524-49810

Query Match 100.0%; Score 22; DB 35; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
Db 457 GACGTTGACACGCGGTTTCT 436

RESULT 13
US-09-933-524A-49810/c
Sequence 49810, Application US/09933524A
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/933,524A
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 09/528,409
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: HY-patent.pl Version 3.1
SEQ ID NO 49810
LENGTH: 467
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(467)
OTHER INFORMATION: n = A,T,C or G
US-09-933-524A-49810

Query Match 100.0%; Score 22; DB 35; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
Db 457 GACGTTGACACGCGGTTTCT 436

RESULT 14
US-60-125-787-430/c
Sequence 430, Application US/60125787
GENERAL INFORMATION:
APPLICANT: Hodgson, David M.
APPLICANT: Lincoln, Stephen E.
APPLICANT: Russo, Frank D.

APPLICANT: Spiro, Peter A.
APPLICANT: Banville, Steve C.
APPLICANT: Bratcher, Shawn R.
APPLICANT: Dufour, Gerard E.
APPLICANT: Cohen, Howard J.
APPLICANT: Rosen, Bruce
APPLICANT: Shah, Purvi
APPLICANT: Chalup, Michael S.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Jones, Anissa L.
APPLICANT: Yu, Jimmy Y.
APPLICANT: Greenawalt, Lila B.
APPLICANT: Panzer, Scott R.
APPLICANT: Roseberry, Ana M.
APPLICANT: Wright, Rachel J.
TITLE OF INVENTION: TRANSCRIPTION FACTOR MOLECULES
FILE REFERENCE: PT-0017 P
CURRENT APPLICATION NUMBER: US/60/125,787
CURRENT FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 591
SOFTWARE: PERL Program
SEQ ID NO 430
LENGTH: 546
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 22091.1
US-60-125-787-430

Query Match 100.0%; Score 22; DB 56; Length 546;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
Db 453 GACGTTGACACGCGGTTTCT 432

RESULT 15
PCT-US01-08631-6785/c
Sequence 6785, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 6785
LENGTH: 2010
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (50)...(1843)
OTHER INFORMATION: 100% homologous to Homo sapiens IGF-II mRNA-binding protein
OTHER INFORMATION: 2,accession number AF117107,Smith-Waterman Scores=3059.
PCT-US01-08631-6785

Query Match 100.0%; Score 22; DB 1; Length 2010;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
Db 421 GACGTTGACACGCGGTTTCT 400

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us-09-270-437d-14.rnpx

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Search completed: April 18, 2003, 09:35:49
Job time : 1213 secs

Mon Apr 21 10:30:44 2003

APPLICANT: Old, Lloyd J.
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen
 TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
 FILE REFERENCE: LUD 5538.1
 CURRENT APPLICATION NUMBER: US/09/270,437D
 CURRENT FILING DATE: 1999-03-16
 PRIOR APPLICATION NUMBER: 09/061,709
 PRIOR FILING DATE: 1998-04-17
 NUMBER OF SEQ ID NOS: 23
 SEQ ID NO 8
 LENGTH: 3283
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3243
 OTHER INFORMATION: unsure of nucleotide

US-09-270-437D-8
 Query Match 100.0%; Score 22; DB 5; Length 3283;
 Best Local Similarity 100.0%; Pred. No. 0.51; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

Qy 1 GACGTTGACACGCGGTTTCT 22
 Db 444 GACGTTGACACGCGGTTTCT 423

RESULT 3
 US-09-270-437D-6/c
 Sequence 6, Application US/09270437D
 GENERAL INFORMATION:
 APPLICANT: Chen, Yao-Tseng
 APPLICANT: Gure, Ali
 APPLICANT: Tsang, Solam
 APPLICANT: Stockert, Elisabeth
 APPLICANT: Jager, Elke
 APPLICANT: Knuth, Alexander
 APPLICANT: Old, Lloyd J.
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigen
 TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
 FILE REFERENCE: LUD 5538.1
 CURRENT APPLICATION NUMBER: US/09/270,437D
 CURRENT FILING DATE: 1999-03-16
 PRIOR APPLICATION NUMBER: 09/061,709
 PRIOR FILING DATE: 1998-04-17
 NUMBER OF SEQ ID NOS: 23
 SEQ ID NO 6
 LENGTH: 3412
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3372
 OTHER INFORMATION: unsure of nucleotide

US-09-270-437D-6
 Query Match 100.0%; Score 22; DB 5; Length 3412;
 Best Local Similarity 100.0%; Pred. No. 0.51; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

Qy 1 GACGTTGACACGCGGTTTCT 22
 Db 444 GACGTTGACACGCGGTTTCT 423

RESULT 4
 US-10-170-235-21870/c
 Sequence 21870, Application US/10170235
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig
 TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
 TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF

FILE REFERENCE: CL001380
 CURRENT APPLICATION NUMBER: US/10/170,235
 CURRENT FILING DATE: 2003-03-17
 NUMBER OF SEQ ID NOS: 42514
 SEQ ID NO 21870
 LENGTH: 3427
 TYPE: DNA
 ORGANISM: HUMAN
 US-10-170-235-21870

Query Match 100.0%; Score 22; DB 8; Length 3427;
 Best Local Similarity 100.0%; Pred. No. 0.52; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

Qy 1 GACGTTGACACGCGGTTTCT 22
 Db 442 GACGTTGACACGCGGTTTCT 421

RESULT 5
 US-60-453-135-3834/c
 Sequence 3834, Application US/60453135
 GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele
 APPLICANT: IAKOUBOVA, Olga
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001456
 CURRENT APPLICATION NUMBER: US/60/453,135
 CURRENT FILING DATE: 2003-03-10
 NUMBER OF SEQ ID NOS: 82762
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3834
 LENGTH: 3427
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-60-453-135-3834

Query Match 100.0%; Score 22; DB 11; Length 3427;
 Best Local Similarity 100.0%; Pred. No. 0.52; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

Qy 1 GACGTTGACACGCGGTTTCT 22
 Db 442 GACGTTGACACGCGGTTTCT 421

RESULT 6
 US-60-453-050-3834/c
 Sequence 3834, Application US/60453050
 GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele
 APPLICANT: LUKE, May
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001457
 CURRENT APPLICATION NUMBER: US/60/453,050
 CURRENT FILING DATE: 2003-03-10
 NUMBER OF SEQ ID NOS: 82762
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3834
 LENGTH: 3427
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-60-453-050-3834

Query Match 100.0%; Score 22; DB 11; Length 3427;
 Best Local Similarity 100.0%; Pred. No. 0.52; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

Qy 1 GACGTTGACACGCGGTTTCT 22
 Db 442 GACGTTGACACGCGGTTTCT 421


```
RESULT 7
US-10-170-235-22086/c
; Sequence 22086, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 22086
; LENGTH: 3475
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-22086

Query Match      100.0%; Score 22; DB 8; Length 3475;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
   |||||
Db 439 GACGTTGACACGCGGTTTCT 418

RESULT 8
US-60-453-135-3835/c
; Sequence 3835, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3835
; LENGTH: 3475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-3835

Query Match      100.0%; Score 22; DB 11; Length 3475;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
   |||||
Db 439 GACGTTGACACGCGGTTTCT 418

RESULT 9
US-60-453-050-3835/c
; Sequence 3835, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3835
; LENGTH: 3475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-050-3835

Query Match      100.0%; Score 22; DB 11; Length 3475;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
   |||||
Db 439 GACGTTGACACGCGGTTTCT 418

RESULT 10
US-60-452-680-30351/c
; Sequence 30351, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30351
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-452-680-30351

Query Match      85.5%; Score 18.8; DB 11; Length 201;
Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
   |||||
Db 135 GACGTTGACACGCGGTTTCT 114

RESULT 11
US-60-452-680-30361/c
; Sequence 30361, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30361
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-452-680-30361

Query Match      85.5%; Score 18.8; DB 11; Length 201;
Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
   |||||
Db 135 GACGTTGACACGCGGTTTCT 114

RESULT 12
US-60-453-135-20375/c
; Sequence 20375, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
```

```
US-60-453-050-3835

Query Match      100.0%; Score 22; DB 11; Length 3475;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
   |||||
Db 439 GACGTTGACACGCGGTTTCT 418

RESULT 10
US-60-452-680-30351/c
; Sequence 30351, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30351
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-452-680-30351

Query Match      85.5%; Score 18.8; DB 11; Length 201;
Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
   |||||
Db 135 GACGTTGACACGCGGTTTCT 114

RESULT 11
US-60-452-680-30361/c
; Sequence 30361, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30361
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-452-680-30361

Query Match      85.5%; Score 18.8; DB 11; Length 201;
Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
   |||||
Db 171 GACGTTGACACGCGGTTTCT 150

RESULT 12
US-60-453-135-20375/c
; Sequence 20375, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
```

Mon Apr 21 10:30:44 2003

us-09-270-437d-14.rnpn

1 GACGTTGACAAACGGCGTTTCT 22
135 GACGTTGACAAACAGTGTTTCT 114

RESULT 15
US-60-453-050-20385/c
; Sequence 20385, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20375
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-20375

Query Match 85.5%; Score 18.8; DB 11; Length 201;
Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACAAACGGCGTTTCT 22
DB 135 GACGTTGACAAACAGTGTTTCT 114

RESULT 13
US-60-453-135-20385/c
; Sequence 20385, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20385
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-20385

Query Match 85.5%; Score 18.8; DB 11; Length 201;
Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACAAACGGCGTTTCT 22
DB 171 GACGTTGACAAACAGTGTTTCT 150

RESULT 14
US-60-453-050-20375/c
; Sequence 20375, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20375
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-050-20375

Query Match 85.5%; Score 18.8; DB 11; Length 201;
Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACAAACGGCGTTTCT 22
DB 135 GACGTTGACAAACAGTGTTTCT 114

RESULT 15
US-60-453-050-20385/c
; Sequence 20385, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20385
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-050-20385

Query Match 85.5%; Score 18.8; DB 11; Length 201;
Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACGTTGACAAACGGCGTTTCT 22
DB 171 GACGTTGACAAACAGTGTTTCT 150

Search completed: April 18, 2003, 10:50:34
Job time : 248.167 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 04:47:40 ; Search time 766 Seconds
(without alignments)
465.145 Million cell updates/sec

Title: US-09-270-437D-14

Perfect score: 22

Sequence: 1 gacgttgacacgsggtttct 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_esti.*

9: gb_esti.*

10: gb_est2.*

11: gb_hic.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_mam.*

24: em_gss_mus.*

25: em_gss_othr.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	100.0	402	12	BG003431
C 2	22	100.0	453	9	AL121466
C 3	22	100.0	531	12	BG0009869
C 4	22	100.0	594	13	B1858380
C 5	22	100.0	620	12	BF914566
C 6	22	100.0	642	17	AQ479871

7	22	100.0	688	17	AG087457
8	22	100.0	724	14	BM977219
9	22	100.0	759	10	BE622021
10	22	100.0	851	14	BQ221568
11	22	100.0	856	12	BG480515
12	22	100.0	889	12	BG748346
13	22	100.0	1089	14	BM806132
14	21	95.5	682	17	AG048517
15	20.4	92.7	448	10	BB852457
16	20.4	92.7	458	10	BB852318
17	20.4	92.7	462	10	BB860142
18	20.4	92.7	469	10	BB853640
19	20.4	92.7	541	14	BQ770242
20	20.4	92.7	629	13	B1655144
21	20.4	92.7	663	10	BB643209
22	20.4	92.7	668	10	BB618315
23	20.4	92.7	815	13	B1688088
24	20.4	92.7	905	13	B1654462
25	19.4	88.2	464	10	BB862701
26	18.8	85.5	489	10	BB855310
27	17.8	80.9	522	12	BG279958
28	17.8	80.9	790	12	BF140399
29	17.8	80.9	1120	17	CNS06502
30	17.2	78.2	329	17	AQ091026
31	17.2	78.2	479	14	BQ028477
32	17.2	78.2	511	9	AI960673
33	17.2	78.2	517	12	BG543604
34	17.2	78.2	522	17	AQ467039
35	17.2	78.2	543	14	BQ026166
36	17.2	78.2	548	17	AZ178687
37	17.2	78.2	555	14	BQ488142
38	17.2	78.2	562	13	EM186239
39	17.2	78.2	576	14	BQ024011
40	17.2	78.2	581	14	BQ025444
41	17.2	78.2	581	14	BQ029203
42	17.2	78.2	616	17	AZ792519
43	17.2	78.2	625	14	BQ025074
44	17.2	78.2	637	10	BE263528
45	17.2	78.2	640	14	BQ027309

ALIGNMENTS

RESULT 1
BG003431/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

402 bp mRNA linear EST 24-JAN-2001
RCI-GN0198-171100-021-f07 GN0198 Homo sapiens cDNA, mRNA sequence.
BG003431
BG003431.1 GI:12443763
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-GN0198-171100-021-f07&t3=2000-11-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 400.

FEATURES
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1..402
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0198"
/dev_stage="Adult"
/note="Organ: placenta normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
117 a 98 c 109 g 78 t

BASE COUNT 117 a 98 c 109 g 78 t
ORIGIN
Query Match 100.0%; Score 22; DB 12; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.2; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 GACGTTGACACGGCGGTTTCT 22
|||||
Db 195 GACGTTGACACGGCGGTTTCT 174

RESULT 2
LOCUS AL121466/c 453 bp mRNA linear EST 25-FEB-2000
DEFINITION DKFZp762L097_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
AL121466
ACCESSION AL121466
VERSION AL121466.1 GI:5927467
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 453)
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: Ottenwaelder B
MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
available.
This clone (DKFZp762L097) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
FEATURES
source
1..453
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DKFZp762L097"
/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (Mewo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPort1; Site_1: NotI; Site_2: SalI"
117 a 121 c 137 g 78 t

ORIGIN

Query Match 100.0%; Score 22; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.5; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 GACGTTGACACGGCGGTTTCT 22
|||||
Db 430 GACGTTGACACGGCGGTTTCT 409

RESULT 3
LOCUS BG009869 531 bp mRNA linear EST 24-JAN-2001
DEFINITION QV1-GN0320-041200-532-c06 GN0320 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG009869
VERSION BG009869.1 GI:12456498
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 531)
AUTHORS Dias Neto,E., Garcia Correa,R., Vertovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV1&t2=QV1-GN0320-
041200-532-c06&t3=2000-12-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 531.
Location/Qualifiers
1..531
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0320"
/dev_stage="Adult"
/note="Organ: placenta normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
104 a 138 c 135 g 154 t

BASE COUNT 104 a 138 c 135 g 154 t
ORIGIN
Query Match 100.0%; Score 22; DB 12; Length 531;
Best Local Similarity 100.0%; Pred. No. 4.9; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 GACGTTGACACGGCGGTTTCT 22
|||||
Db 339 GACGTTGACACGGCGGTTTCT 360

FEATURES

source
1..531
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0320"
/dev_stage="Adult"
/note="Organ: placenta normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
104 a 138 c 135 g 154 t

BASE COUNT

Query Match 100.0%; Score 22; DB 12; Length 531;
Best Local Similarity 100.0%; Pred. No. 4.9; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 GACGTTGACACGGCGGTTTCT 22
|||||
Db 339 GACGTTGACACGGCGGTTTCT 360

RESULT 4

BI858380/c
 LOCUS 603383965F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5392792 5',
 DEFINITION mRNA sequence.
 ACCESSION BI858380
 VERSION BI858380.1 GI:15999127
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 594)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue procurement: DCTD/DTF
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM12001 row: a column: 17
 High quality sequence stop: 594.
 Location/Qualifiers
 1..594
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5392792"
 /tissue_type="mammary adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: breast; Vector: PCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
 Average insert size 1.383 Kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH MGC Library."
 167 a 157 c 150 g 120 t
 BASE COUNT 167 a 157 c 150 g 120 t
 ORIGIN
 Query Match 100.0%; Score 22; DB 13; Length 594;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GACGTTGACACGCGGGTTTCT 22
 ||||||||||||||||||
 Db 197 GACGTTGACACGCGGGTTTCT 176
 RESULT 5
 BF914566/c
 LOCUS IL3-UT0114-011200-362-E06 UT0114 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BF914566
 VERSION BF914566.1 GI:12306024
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 620)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663

COMMENT
 Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t=IL3-UT0114-011200-362-E06&t3=2000-12-01&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 619.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="UT0114"
 /dev_stage="Adult"
 /note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 181 a 157 c 150 g 132 t
 BASE COUNT 181 a 157 c 150 g 132 t
 ORIGIN
 Query Match 100.0%; Score 22; DB 12; Length 620;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GACGTTGACACGCGGGTTTCT 22
 ||||||||||||||||||
 Db 385 GACGTTGACACGCGGGTTTCT 364
 RESULT 6
 AQ479871
 LOCUS RPCI-11-274C8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-274C8,
 DEFINITION DNA sequence.
 ACCESSION AQ479871
 VERSION AQ479871.1 GI:4661990
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 642)
 AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
 J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@igr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genet ca (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers

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source
1. .642
/organism="Homo sapiens"
/db_xref="GDB:7604887"
/db_xref="taxon:9606"
/clone_lib="RPCL-11"
/sex="Male"
/cell_type="Lymphocytes"
/notes="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
RPC11 Human Male BAC Library"
BASE COUNT 207 a 117 c 95 g 223 t
ORIGIN
Query Match 100.0%; Score 22; DB 17; Length 642;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGGCGGTTTCT 22
|||||
Db 76 GACGTTGACACGGCGGTTTCT 97

RESULT 7
AG087457 688 bp DNA linear GSS 03-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-086B21.F, genomic survey sequence.
ACCESSION AG087457
VERSION AG087457.1 GI:16639259
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-086B21.F.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
2 (bases 1 to 688)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbegsc.riken.go.jp, URL:http://bgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1. .688
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone_lib="PTB-086B21.F"
/sex="male"
/cell_type="lymphoblast"
/cell_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 217 a 153 c 120 g 198 t
ORIGIN
Query Match 100.0%; Score 22; DB 17; Length 688;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGGCGGTTTCT 22
|||||
Db 87 GACGTTGACACGGCGGTTTCT 66

Db 321 GACGTTGACACGGCGGTTTCT 342
|||||
RESULT 8
BM977219 724 bp mRNA linear EST 21-MAR-2002
LOCUS UI-CF-DUI-ads-n-12-0-UI.81 UI-CF-DUI Homo sapiens cDNA clone
DEFINITION UI-CF-DUI-ads-n-12-0-UI 3', mRNA sequence.
ACCESSION BM977219
VERSION BM977219.1 GI:19595413
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 724)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE 97044477
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1. .724
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UI-CF-DUI-ads-n-12-0-UI"
/clone_lib="UI-CF-DUI"
/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/notes="Organ: Lung; Vector: pTV3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-DUI is a normalized cDNA library containing the
following tissue(s): Primary Lung Epithelial Cells The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pTV3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (GT)18 tail. The sequence tag for this
library is GGCTGTAGGC.
TAG LIB=UI-CF-DUI
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_SEQ=GGCTGTAGGC"
BASE COUNT 219 a 174 c 182 g 149 t
ORIGIN
Query Match 100.0%; Score 22; DB 14; Length 724;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACGTTGACACGGCGGTTTCT 22
|||||
Db 87 GACGTTGACACGGCGGTTTCT 66

```

```

RESULT 9
BB622021/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BB622021
601440873F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915546 5',
mRNA sequence.
EST.
BB622021.1 GI:9892961
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 759)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9739 row: a column: 19
High quality sequence stop: 622.
Location/Qualifiers
1..759
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:3915546"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 228 a 209 c 188 g 134 t
ORIGIN
1..759
GACGTTGACACGCGGTTTCT 22
|||||
GACGTTGACACGCGGTTTCT 143

Query Match 100.0%; Score 22; DB 10; Length 759;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
GACGTTGACACGCGGTTTCT 143

Db 164 GACGTTGACACGCGGTTTCT 143

RESULT 10
BQ221568/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BQ221568
7559207 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6046477
5', mRNA sequence.
EST.
BQ221568.1 GI:20402968
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 851)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9739 row: a column: 19
High quality sequence stop: 622.
Location/Qualifiers
1..851
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:6046477"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 229 a 234 c 231 g 157 t
ORIGIN
1..851
GACGTTGACACGCGGTTTCT 22
|||||
GACGTTGACACGCGGTTTCT 377

Query Match 100.0%; Score 22; DB 14; Length 851;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
GACGTTGACACGCGGTTTCT 377

Db 398 GACGTTGACACGCGGTTTCT 377

RESULT 11
BG480515/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BG480515
602529520F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4652981 5',
mRNA sequence.
EST.
BG480515.1 GI:13412705
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 856)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: ATCC
cDNA Library Arrayed by: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9739 row: h column: 06
High quality sequence stop: 661.
Location/Qualifiers
1..856
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:4652981"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit

```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM13292 row: f column: 14
 High quality sequence stop: 637.
 Location/Qualifiers
 1..851
 /organism="Homo sapiens"
 /db xref="taxon:9606"
 /clone="IMAGE:6046477"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

```

BASE COUNT 229 a 234 c 231 g 157 t
ORIGIN
1..851
GACGTTGACACGCGGTTTCT 22
|||||
GACGTTGACACGCGGTTTCT 377

Query Match 100.0%; Score 22; DB 14; Length 851;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
GACGTTGACACGCGGTTTCT 377

Db 398 GACGTTGACACGCGGTTTCT 377

```

```

RESULT 11
BG480515/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BG480515
602529520F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4652981 5',
mRNA sequence.
EST.
BG480515.1 GI:13412705
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 856)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: ATCC
cDNA Library Arrayed by: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1438 row: h column: 06
High quality sequence stop: 661.
Location/Qualifiers
1..856
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:4652981"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit

```

```

BASE COUNT 229 a 234 c 231 g 157 t
ORIGIN
1..851
GACGTTGACACGCGGTTTCT 22
|||||
GACGTTGACACGCGGTTTCT 377

Query Match 100.0%; Score 22; DB 14; Length 851;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGTTGACACGCGGTTTCT 22
|||||
GACGTTGACACGCGGTTTCT 377

Db 398 GACGTTGACACGCGGTTTCT 377

```

BM806132	GI:19122955
BM806132.1	GI:19122955
EST.	
human.	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
1 (bases 1 to 1089)	
NIH-MGC http://mgc.ncbi.nlm.nih.gov/ .	
National Institutes of Health, Mammalian Gene Collection (MGC)	
Unpublished (1999)	
Contact: Robert Strausberg, Ph.D.	
Email: cgapbs-remail.nih.gov	
Tissue Procurement: ATCC	
CDNA Library Preparation: Life Technologies, Inc.	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Agencourt Bioscience Corporation	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	
http://image.llnl.gov	
Plate: LLAM12276 row: c column: 13	
High quality sequence stop: 688.	
Location/Qualifiers	
1. .1089	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:555652"	
/clone_lib="NIH MGC 71"	
/tissue_type="leiomyosarcoma"	
/lab_host="PH10B (phage-resistant)"	
/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.	
Average insert size 2.1 kb.	
1 others	
BASE COUNT	315 a 280 c 272 g 221 t
ORIGIN	
Query Match	100.0%; Score 22; DB 14; Length 1089;
Best Local Similarity	100.0%; Pred. No. 7,2;
Matches 22; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACGTTGACACGCGGTTTCT 22	
Db 244 GACGTTGACACGCGGTTTCT 223	
RESULT 14	
AG048517	682 bp DNA linear GSS 02-NOV-2001
LOCUS	Pan troglodytes DNA, clone: PTB-028F21.F, genomic survey sequence.
DEFINITION	
ACCESSION	AG048517
VERSION	AG048517.1 GI:16585409
KEYWORDS	GSS.
SOURCE	Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-028F21.F.
ORGANISM	Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	
1	
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Tokoki,Y., Watanabe,H. and Sakaki,Y.	
BAC end sequences of library PTB	
Unpublished	
2 (bases 1 to 682)	
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Tokoki,Y., Watanabe,H. and Sakaki,Y.	
Direct Submission	
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimbpe@gsc.riken.go.jp , URL: http://hgp.gsc.riken.go.jp/ , Tel:81-45-503-9111, Fax:81-45-503-9170)	
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. .682

/organism="Pan troglodytes"

/db_xref="taxon:9598"

/clone="PTB-028F21.F"

/sex="male"

/cell_type="lymphoblast"

/clone_lib="PTB Chimpanzee Male BAC Library"

217 a 147 c 112 g 199 t 7 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

21; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY 1 GAGCTTGACACGGCGGTTTCT 22

DB 255 GAGCTTGACACGGCGGTTTCT 276

BB852457

BB852457

BB852457

BB852457

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Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001). Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers

1. .448

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="G370007124"

/cell_lib="RIKEN full-length enriched, B16 F10Y cells"

/note="pooled tissues; (tissue type=cerebellum, dev stage=16 days neonate, sex=mixed), (tissue type=cerebellum, dev stage=0 day neonate, sex=mixed), (tissue type=hippocampus, dev stage=adult, sex=male), (tissue type=whole body, dev stage=9 days embryo, sex=mixed), (tissue type=lung, dev stage=13 days embryo, sex=mixed)"

BASE COUNT 113 a 119 c 141 g 75 t

ORIGIN

Query Match

Best Local Similarity

Matches

21; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY 1 GAGCTTGACACGGCGGTTTCT 22

DB 420 GAGCTTGACACGGCGGTTTCT 399

Search completed: April 18, 2003, 07:32:04

Job time : 769.167 secs

clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. .682

/organism="Pan troglodytes"

/db_xref="taxon:9598"

/clone="PTB-028F21.F"

/sex="male"

/cell_type="lymphoblast"

/clone_lib="PTB Chimpanzee Male BAC Library"

217 a 147 c 112 g 199 t 7 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

21; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY 1 GAGCTTGACACGGCGGTTTCT 22

DB 255 GAGCTTGACACGGCGGTTTCT 276

BB852457

BB852457

BB852457

BB852457

BB852457

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BB852457

BB852457

clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. .682

/organism="Pan troglodytes"

/db_xref="taxon:9598"

/clone="PTB-028F21.F"

/sex="male"

/cell_type="lymphoblast"

/clone_lib="PTB Chimpanzee Male BAC Library"

217 a 147 c 112 g 199 t 7 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

21; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY 1 GAGCTTGACACGGCGGTTTCT 22

DB 255 GAGCTTGACACGGCGGTTTCT 276

BB852457

BB852457

BB852457

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BB852457

